

09/1899 295 Page 1
Seq. ID 2 w/ inter

OM Protein - protein search, using sw model
 Run on: June 30, 2003, 16:16:45 ; Search time 311 Seconds
 (without alignments)
 744.242 Million cell updates/sec

Perfect score: US-09-899-295-2
 Sequence: 1 MTLESTMACCLSEEKAREARR... VFAAVKDTIQLQLNKEYNLV 359

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 641733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1860	100.0	359	21 US-09-791-537-57305 Sequence 57305, A
2	1860	100.0	359	22 US-09-899-295-2 Sequence 2, Appli
3	1857	99.8	359	18 US-09-471-572-8 Sequence 8, Appli
4	1857	99.8	359	21 US-09-791-537-51282 Sequence 81282, A
5	1849	99.4	359	18 US-09-471-572-7 Sequence 81282, A
6	1849	.99.4	359	21 US-09-791-537-78690 Sequence 78690, A

RESULT 1
 US-09-791-537-57305
 ; Sequence 57305, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomics, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Dancer, Joseph
 ; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 57305
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-791-537-57305

ALIGMENTS

SEQUENCE ALIGNMENT

Query Match 100.0% ; Score 1860; DB 21; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.1e-175; Indels 0; Gaps 0;

Matches 359: Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

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 Db 1 MTLESTMACCLSEEKAREARR... VFAAVKDTIQLQLNKEYNLV 359
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61 IIRGSGYSDEDKRGFTKLYQNTIAMQAMIRAMDTLKIPIYEHNKAHQVLREVDEK 120
 Db 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 Db 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 .181 RSVRPTGIEYPDFQSLQSVIFRMVDDGQGQSRERRKWHCENVTISIMLVALESDQVLV 240
 Qy 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Db 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Qy 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359
 Db 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359
 RESULT 2
 US-09-899-295-2
 ; Sequence 2, Application US/09899295
 ; GENERAL INFORMATION:
 ; APPLICANT: Aventis Pharma Deutschland GmbH
 ; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
 ; TITLE OF INVENTION: receptors
 ; FILE REFERENCE: AVE D-2000/A033 englisch
 ; CURRENT APPLICATION NUMBER: US/09/899,295
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 Query Match 100.0%; Score 1860; DB 22; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1..1e-175;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTLESIMACCLSEEAKEARRINDEIERHVRDRKDARRELKLILLGTGESGKSTIKOMR 60
 Db 1 MTLESIMACCLSEEAKEARRINDEIERHVRDRKDARRELKLILLGTGESGKSTIKOMR 60
 Qy 61 IIHGSGYSDEDKRGFTKLYQNTIAMQAMIRAMDTLKIPIYEHNKAHQVLREVDEK 120
 Db 61 IIHGSGYSDEDKRGFTKLYQNTIAMQAMIRAMDTLKIPIYEHNKAHQVLREVDEK 120
 Qy 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 Db 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 .181 RSVRPTGIEYPDFQSLQSVIFRMVDDGQGQSRERRKWHCENVTISIMLVALESDQVLV 240
 Qy 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Db 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Qy 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359
 Db 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359
 RESULT 3
 US-09-471-572-8
 ; Sequence 8, Application US/09471572
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Kenneth A.
 ; APPLICANT: Walker, Mary W.
 ; ORGANISM: Mus musculus
 Query Match 99.8%; Score 1857; DB 21; Length 359;
 Best Local Similarity 99.7%; Pred. No. 2..1e-175;
 Matches 358; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTLESIMACCLSEEAKEARRINDEIERHVRDRKDARRELKLILLGTGESGKSTIKOMR 60
 Db 1 MTLESIMACCLSEEAKEARRINDEIERHVRDRKDARRELKLILLGTGESGKSTIKOMR 60
 Qy 61 IIHGSGYSDEDKRGFTKLYQNTIAMQAMIRAMDTLKIPIYEHNKAHQVLREVDEK 120
 Db 61 IIHGSGYSDEDKRGFTKLYQNTIAMQAMIRAMDTLKIPIYEHNKAHQVLREVDEK 120
 Qy 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 Db 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 .181 RSVRPTGIEYPDFQSLQSVIFRMVDDGQGQSRERRKWHCENVTISIMLVALESDQVLV 240
 Qy 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Db 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Qy 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359
 Db 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359
 RESULT 4
 US-09-791-537-81282
 ; Sequence 81282, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; APPLICANT: Dere, Derek
 ; APPLICANT: Bionomix, Inc.
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791.537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 81282
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 Query Match 99.8%; Score 1857; DB 21; Length 359;
 Best Local Similarity 99.7%; Pred. No. 2..1e-175;
 Matches 358; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTLESIMACCLSEEAKEARRINDEIERHVRDRKDARRELKLILLGTGESGKSTIKOMR 60
 Db 1 MTLESIMACCLSEEAKEARRINDEIERHVRDRKDARRELKLILLGTGESGKSTIKOMR 60
 Qy 61 IIHGSGYSDEDKRGFTKLYQNTIAMQAMIRAMDTLKIPIYEHNKAHQVLREVDEK 120
 Db 61 IIHGSGYSDEDKRGFTKLYQNTIAMQAMIRAMDTLKIPIYEHNKAHQVLREVDEK 120
 Qy 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 Db 121 VSAFENPYVDAIKSLWNPQIQCYDRREYQOLSDSTKYLNDLDRVADPAVLPTQDVL 180
 .181 RSVRPTGIEYPDFQSLQSVIFRMVDDGQGQSRERRKWHCENVTISIMLVALESDQVLV 240
 Qy 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Db 241 ESDNENRMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMSHLVYFPEYDQQR 300
 Qy 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359
 Db 301 DAQAAREFILKMFVLDNPDSDKLIYSHFTCATDTENIREVFAAVKDTIQLNLKEYLV 359

RESULT 5

US-09-471-572-7

; Sequence 7, Application US/09471572

; GENERAL INFORMATION:

; APPLICANT: Jones, Kenneth A.

; APPLICANT: Walker, Mary W.

; APPLICANT: Tatum, Joseph A.

; APPLICANT: Branchek, Theresa A.

; APPLICANT: Gerald, Christophe P.G.

; TITLE OF INVENTION: Chimeric G-Proteins And Uses Thereof

; FILE REFERENCE: 59896

; CURRENT APPLICATION NUMBER: US/09/471,572

; CURRENT FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 359

; TYPE: PRT

; ORGANISM: Canis familiaris

US-09-471-572-7

Query Match 99.4%; Score 1849; DB 18; Length 359; Best Local Similarity 99.4%; Pred. No. 1; 3e-174; 1; Mismatches 0; Indels 0; Gaps 0; Matches 357; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.4%; Score 1849; DB 21; Length 359; Best Local Similarity 99.4%; Pred. No. 1; 3e-174; 1; Mismatches 1; Indels 0; Gaps 0; Matches 357; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MILESIMACCLSEEAKARRINDEIERVVRDKRDRARRELKLILLGGESEKSTFIKMR 60

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Db 61 IHGSGSDEDKRKGFTKLUVQNTFTAMQAMIRAMDTKIPKYEHNKHAQLYREVDEK 120

QY 121 VSAFENPYVDAIKSLWNDPGIQEYDRREYOLSDSTKYLNDDRDPAVLPTQDVL 180

Db 121 VSAFENPYVDAIKSLWNDPGIQEYDRREYOLSDSTKYLNDDRDPAVLPTQDVL 180

QY 181 RVRVPPTGIEYFPDLSQVIFRMWDVGGORSERRMKWHCFENVTIMFLVALSEYDQVL 240

Db 181 RVRVPPTGIEYFPDLSQVIFRMWDVGGORSERRMKWHCFENVTIMFLVALSEYDQVL 240

QY 301 DQAAREFILKMFVLDNPDSDKIYSHFTCATDENTIRVFAAVKDTIQLNLKEYNLV 359

Db 301 DQAAREFILKMFVLDNPDSDKIYSHFTCATDENTIRVFAAVKDTIQLNLKEYNLV 359

QY 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDLLEKIMSHLYDYPEYDQQR 300

Db 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDLLEKIMSHLYDYPEYDQQR 300

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Db 1 MILESIMACCLSEEAKARRINDEIERVVRDKRDRARRELKLILLGGESEKSTFIKMR 60

QY 61 IHGSGSDEDKRKGFTKLUVQNTFTAMQAMIRAMDTKIPKYEHNKHAQLYREVDEK 120

Db 61 IHGSGSDEDKRKGFTKLUVQNTFTAMQAMIRAMDTKIPKYEHNKHAQLYREVDEK 120

QY 121 VSAFENPYVDAIKSLWNDPGIQEYDRREYOLSDSTKYLNDDRDPAVLPTQDVL 180

Db 121 VSAFENPYVDAIKSLWNDPGIQEYDRREYOLSDSTKYLNDDRDPAVLPTQDVL 180

QY 181 RVRVPPTGIEYFPDLSQVIFRMWDVGGORSERRMKWHCFENVTIMFLVALSEYDQVL 240

Db 181 RVRVPPTGIEYFPDLSQVIFRMWDVGGORSERRMKWHCFENVTIMFLVALSEYDQVL 240

QY 301 DQAAREFILKMFVLDNPDSDKIYSHFTCATDENTIRVFAAVKDTIQLNLKEYNLV 359

Db 301 DQAAREFILKMFVLDNPDSDKIYSHFTCATDENTIRVFAAVKDTIQLNLKEYNLV 359

QY, 1 MILESIMACCLSEEAKARRINDEIERVVRDKRDRARRELKLILLGGESEKSTFIKMR 60

QY, ; Sequence 78690, Application US/09791537

RESULT 6

US-09-791-537-78690

Query Match 99.2%; Score 1846; DB 1; Length 359; Best Local Similarity 99.2%; Pred. No. 2; 6e-174; 1; Indels 0; Gaps 0; Matches 356; Conservative 2; Mismatches 1;

QY, 1 MILESIMACCLSEEAKARRINDEIERVVRDKRDRARRELKLILLGGESEKSTFIKMR 60

ORGANISM: Mus sp.
US-09-989-497-1

Query Match 99.2%; Score 1846; DB 23; Length 359;
Best Local Similarity 99.2%; Pred. No. 2.6e-174;
Matches 356; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 181 RVVPTGIEYPFDLQSVIFRMDVGQCSRERRKWHCFCENVTSMPLVALSEYDQVL 240

Db 181 RVVPTGIEYPFDLQSVIFRMDVGQCSRERRKWHCFCENVTSMPLVALSEYDQVL 240

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Db 241 ESDNENRMEESKALFRTITYWFQNSVILFLNKDLEEKIMYSHLVDYFPEYDQPR 300

QY 301 DAQAREFLKMFVLDNPDSDKTIYSHFTCAATTENIRFVFAAKDTILQNLKEYNV 359
301 DAQAREFLKMFVLDNPDSDKTIYSHFTCAATTENIRFVFAAKDTILQNLKEYNV 359

Db 301 DAQAREFLKMFVLDNPDSDKTIYSHFTCAATTENIRFVFAAKDTILQNLKEYNV 359

RESULT 11
US-09-791-537-72283

; Sequence 72283, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791, 537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-471-572-6

Query Match 99.1%; Score 1844; DB 18; Length 359;
Best Local Similarity 99.2%; Pred. No. 4.1e-174;
Matches 356; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTLIESIMACCLSEAKERARRINDEIERVRROKDRARRELKULLLGGESEKSTFKQMR 60
1 MTLIESIMACCLSEAKERARRINDEIERVRROKDRARRELKULLLGGESEKSTFKQMR 60

Db 61 IHGSGSDEDKRGFTKLVQNIFTAMQAMIRAMDTLKIPYKEHNKAQALVREDEVK 120

QY 121 VSAFENYVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180

Db 121 VSAFENYVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180

QY 181 RVVPTGIEYPFDLQSVIFRMDVGQCSRERRKWHCFCENVTSMPLVALSEYDQVL 240

Db 181 RVVPTGIEYPFDLQSVIFRMDVGQCSRERRKWHCFCENVTSMPLVALSEYDQVL 240

QY 241 ESDNENRMEESKALFRTITYWFQNSVILFLNKDLEEKIMYSHLVDYFPEYDQPR 300

Db 241 ESDNENRMEESKALFRTITYWFQNSVILFLNKDLEEKIMYSHLVDYFPEYDQPR 300

QY 301 DAQAREFLKMFVLDNPDSDKTIYSHFTCAATTENIRFVFAAKDTILQNLKEYNV 359
301 DAQAREFLKMFVLDNPDSDKTIYSHFTCAATTENIRFVFAAKDTILQNLKEYNV 359

RESULT 13
US-09-791-537-95492

; Sequence 95492, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791, 537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 95492

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

run on: June 30, 2003, 16:18:06 ; Search time 50 Seconds (without alignments)
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 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 1197705 seqs, 260451061 residues

total number of hits satisfying chosen parameters: 1197705

post-processing: Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Pending Patents AA_New:*

Maximum Match 100%
 Listing first 45 summaries

result No. Score Query Length DB ID Description

1	1849	99.4	359	6	US-10-405-027-3227	Sequence 3227, AP
2	1849	99.4	359	7	US-60-453-135-10419	Sequence 10419, A
3	1849	99.4	359	7	US-60-453-050-10419	Sequence 10419, A
4	1849	99.4	359	7	US-60-445-459-5597	Sequence 5597, AP
5	1849	99.4	359	7	US-60-445-241-5597	Sequence 5597, AP
6	1849	99.4	359	7	US-60-456-412-10419	Sequence 10419, A
7	1844	99.1	359	6	US-10-288-561-2	Sequence 2, Appl
8	1817	97.7	353	1	PCT-US03-02422-13	Sequence 13, Appl
9	1817	97.7	353	6	US-10-552-843-13	Sequence 13, Appl
10	1687	90.7	387	5	US-09-724-676-49632	Sequence 49632, A
11	1687	90.7	387	5	US-09-744-678A-49632	Sequence 49632, A
12	1657	89.1	351	5	US-09-949-01-7853	Sequence 7853, AP
13	1535	82.5	355	6	US-10-326-896-2	Sequence 2, Appl
14	1513	81.1	355	1	PCT-US03-02422-12	Sequence 12, Appl
15	1513	81.3	355	6	US-10-359-493-4982	Sequence 4982, AP
16	1513	81.3	355	6	US-10-352-843-12	Sequence 12, Appl
17	1104	59.4	252	5	US-09-949-016-9408	Sequence 9408, AP
18	1066	57.3	374	5	US-09-448-002-4	Sequence 4, Appl
19	1066	57.3	374	6	US-10-319-416-2	Sequence 2, Appl
20	1055	56.7	374	6	US-10-319-442-20	Sequence 20, Appl
21	1055	56.7	374	6	US-10-414-797-20	Sequence 20, Appl
22	1044	56.1	374	5	US-09-468-002-2	Sequence 2, Appl
23	1044	56.1	378	5	US-09-949-016-7851	Sequence 7851, AP
24	1033	55.5	374	6	US-10-319-416-4	Sequence 4, Appl
25	898.5	48.3	354	1	PCT-US03-02452-14	Sequence 14, Appl
26	898.5	48.3	354	6	US-10-312-833-14	Sequence 14, Appl

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-10-405-027-3227

; Sequence 3227, Application US/10405027

; GENERAL INFORMATION:

; APPLICANT: Rosen et. al.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS805P1

; CURRENT APPLICATION NUMBER: US/10/405, 027

; CURRENT FILING DATE: 2003-04-07

; PRIOR APPLICATION NUMBER: 60/369, 608

; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: 60/376, 175

; PRIOR FILING DATE: 2002-04-30

; NUMBER OF SEQ ID NOS: 5810

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3227

; LENGTH: 359

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-405-027-3227

Query Match 99.4%; Score 1849; DB 6; Length 359;

Best Local Similarity 99.4%; Pred. No. 4.1e-183; Matches 357; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLESIMACCLSEEKAREARRINDEBERHVRDXRDRARREBLKLILLGIGESGSTFKQMR 60

Db 1 MTLESIMACCLSEEKAREARRINDEBERHVRDXRDRARREBLKLILLGIGESGSTFKQMR 60

QY 61 IIHGSYSIDEDKRGFTKLVQNYQFTAMQAMIRAMDTLKIPIKYEHNKHAQULREVDEK 120

Db 61 IIHGSYSIDEDKRGFTKLVQNYQFTAMQAMIRAMDTLKIPIKYEHNKHAQULREVDEK 120

QY 181 RVRYFTTGLEYPDLQSVIFRMWDVGCGRSRKWICFENNTSIMPVALSEYDQVLY 240

Db 181 RVRYFTTGLEYPDLQSVIFRMWDVGCGRSRKWICFENNTSIMPVALSEYDQVLY 240

QY 121 VSAFENPYDAIKSIWNDPGIQECDYDRREYQLSDSLTKVYLNDIDRVADPAVLPTQDVL 180

Db 121 VSAFENPYDAIKSIWNDPGIQECDYDRREYQLSDSLTKVYLNDIDRVADPAVLPTQDVL 180

QY 241 ESDNENRMEESKAFLRTIITYPWFQNSVYILFLNKDLEEKIMSHLYDPEYDGPOR 300

Db 241 ESDNENRMEESKAFLRTIITYPWFQNSVYILFLNKDLEEKIMSHLYDPEYDGPOR 300

QY 301 DAQAREFILKMFVLDNPDSDKITYSHFTCATDTEINRREVFAVAKDTIQLQNLKEYNLV 359

Db 301 DAQAREFILKMFVLDNPDSDKITYSHFTCATDTEINRREVFAVAKDTIQLQNLKEYNLV 359

DAQAREFILKMFVLDNPDSDKITYSHFTCATDTEINRREVFAVAKDTIQLQNLKEYNLV 359

RESULT 2
 US-60-453-135-10419
 Sequence 10419, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01456
 ; CURRENT APPLICATION NUMBER: US/60/453, 135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 10419
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-453-135-10419

Query Match 99.4%; Score 1849; DB 7; Length 359;
 Best Local Similarity 99.4%; Pred. No. 4.1e-183;
 Matches 357; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 Db 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 QY 61 IIHGSYSDEDKRGFTKLVQNYITAMQAMIRAMDTLKIPIKYEHNAHQVREYDVER 120
 Db 61 IIHGSYSDEDKRGFTKLVQNYITAMQAMIRAMDTLKIPIKYEHNAHQVREYDVER 120
 QY 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 Db 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 QY 61 IIHGSYSDEDKRGFTKLVQNYITAMQAMIRAMDTLKIPIKYEHNAHQVREYDVER 120
 Db 61 IIHGSYSDEDKRGFTKLVQNYITAMQAMIRAMDTLKIPIKYEHNAHQVREYDVER 120
 QY 121 VSAFENPYVDAIKSLWNPDQIQCYDRREYQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 Db 121 VSAFENPYVDAIKSLWNPDQIQCYDRREYQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 QY 181 RVRVPTGIEYPFDLQSVIFRMVWGGQSERRWWIHCENVTSMFLVALSEYDQVLV 240
 Db 181 RVRVPTGIEYPFDLQSVIFRMVWGGQSERRWWIHCENVTSMFLVALSEYDQVLV 240
 QY 241 ESDNENRMEESKALFRITIYPWFQNSVILFLNKDLLEKIMSHLVDFPEYDGPOR 300
 Db 241 ESDNENRMEESKALFRITIYPWFQNSVILFLNKDLLEKIMSHLVDFPEYDGPOR 300
 QY 301 DAQAAREFILKMFVLDNPDSDKIYSHFTCATDNTIRFVAVKDTIQLNLKEYNLV 359
 Db 301 DAQAAREFILKMFVLDNPDSDKIYSHFTCATDNTIRFVAVKDTIQLNLKEYNLV 359

RESULT 4
 US-60-456-444-5597
 ; Sequence 5597, Application US/60455444
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BEGOVICH, Ann
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01455
 ; CURRENT APPLICATION NUMBER: US/60/455, 444
 ; CURRENT FILING DATE: 2003-03-18
 ; NUMBER OF SEQ ID NOS: 50986
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5597
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-455-444-5597

Query Match 99.4%; Score 1849; DB 7; Length 359;
 Best Local Similarity 99.4%; Pred. No. 4.1e-183;
 Matches 357; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 Db 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 QY 61 IIHGSYSDEDKRGFTKLVQNYITAMQAMIRAMDTLKIPIKYEHNAHQVREYDVER 120
 Db 61 IIHGSYSDEDKRGFTKLVQNYITAMQAMIRAMDTLKIPIKYEHNAHQVREYDVER 120
 QY 121 VSAFENPYVDAIKSLWNPDQIQCYDRREYQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 Db 121 VSAFENPYVDAIKSLWNPDQIQCYDRREYQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 QY 181 RVRVPTGIEYPFDLQSVIFRMVWGGQSERRWWIHCENVTSMFLVALSEYDQVLV 240
 Db 181 RVRVPTGIEYPFDLQSVIFRMVWGGQSERRWWIHCENVTSMFLVALSEYDQVLV 240
 QY 241 ESDNENRMEESKALFRITIYPWFQNSVILFLNKDLLEKIMSHLVDFPEYDGPOR 300
 Db 241 ESDNENRMEESKALFRITIYPWFQNSVILFLNKDLLEKIMSHLVDFPEYDGPOR 300

RESULT 5
 Query Match 99.4%; Score 1849; DB 7; Length 359;
 Best Local Similarity 99.4%; Pred. No. 4.1e-183;
 Matches 357; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 Db 1 MTLESIMACCLSEEAKARRINDEIERVRDKDARRELKLILLGTGESKSTFKOMR 60
 QY 301 DAQAAREFILKMFVLDNPDSDKIYSHFTCATDNTIRFVAVKDTIQLNLKEYNLV 359
 Db 301 DAQAAREFILKMFVLDNPDSDKIYSHFTCATDNTIRFVAVKDTIQLNLKEYNLV 359

US-60-465-241-5597
 Sequence 5597, Application US/60465241
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: BREGOVICH, Ann
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001468
 ; CURRENT APPLICATION NUMBER: US/60/465,241
 ; CURRENT FILING DATE: 2003-04-23
 ; NUMBER OF SEQ ID NOS: 258418
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 5597
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-465-241-5597

Query Match 99.4%; Score 1849; DB 7; Length 359;
 Best Local Similarity 99.4%; Pred. No. 4.1e-183; Mismatches 1; Indels 0; Gaps 0;
 Matches 357; Conservative

QY 1 MTLESIMACCLSEAKERARRINDEIERVRRDKDARRELKULLLGGESGKSTFIQMR 60
 Db 1 MTLESIMACCLSEAKERARRINDEIERVRRDKDARRELKULLLGGESGKSTFIQMR 60
 Qy 61 IHGSGYSDEDKRKGFTKLVQNFITAMQAMIRAMDTLKIPIYKEHNKAHAOLVREDEVKE 120
 Db 61 IHGSGYSDEDKRKGFTKLVQNFITAMQAMIRAMDTLKIPIYKEHNKAHAOLVREDEVKE 120
 Qy 121 VSAFENPVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180
 Db 121 VSAFENPVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180
 Qy 181 RVVPPTGIEPFDLSQVIFRMDVGQCSRERRKWHCFCENVTSMFLVALSEYDQVL 240
 Db 181 RVVPPTGIEPFDLSQVIFRMDVGQCSRERRKWHCFCENVTSMFLVALSEYDQVL 240
 Qy 301 DAOARETILKMDVLNPDSDKITYSHTCATDTENIRFVFAVKDITLQNLKEYNLV 359
 Db 301 DAOARETILKMDVLNPDSDKITYSHTCATDTENIRFVFAVKDITLQNLKEYNLV 359

RESULT 6
 US-60-466-11-10419
 Sequence 10419, Application US/60466412
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOPOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001466
 ; CURRENT APPLICATION NUMBER: US/60/466,412
 ; CURRENT FILING DATE: 2003-04-30
 ; NUMBER OF SEQ ID NOS: 429241
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 10419
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-466-11-10419

Query Match 99.1%; Score 1844; DB 6; Length 359;
 Best Local Similarity 98.9%; Pred. No. 1.4e-182; Mismatches 2; Indels 0; Gaps 0;
 Matches 355; Conservative

QY 1 MTLESIMACCLSEAKERARRINDEIERVRRDKDARRELKULLLGGESGKSTFIQMR 60
 Db 1 MTLESIMACCLSEAKERARRINDEIERVRRDKDARRELKULLLGGESGKSTFIQMR 60
 Qy 61 IHGSGYSDEDKRKGFTKLVQNFITAMQAMIRAMDTLKIPIYKEHNKAHAOLVREDEVKE 120
 Db 61 IHGSGYSDEDKRKGFTKLVQNFITAMQAMIRAMDTLKIPIYKEHNKAHAOLVREDEVKE 120
 Qy 121 VSAFENPVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180
 Db 121 VSAFENPVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180
 Qy 181 RVVPPTGIEPFDLSQVIFRMDVGQCSRERRKWHCFCENVTSMFLVALSEYDQVL 240
 Db 181 RVVPPTGIEPFDLSQVIFRMDVGQCSRERRKWHCFCENVTSMFLVALSEYDQVL 240
 Qy 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDYFPEYDGPQR 300
 Db 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDYFPEYDGPQR 300
 Qy 301 DAOARETILKMDVLNPDSDKITYSHTCATDTENIRFVFAVKDITLQNLKEYNLV 359
 Db 301 DAOARETILKMDVLNPDSDKITYSHTCATDTENIRFVFAVKDITLQNLKEYNLV 359

RESULT 7
 US-10-258-561-2
 Sequence 2, Application US/10258561
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Kathleen
 ; APPLICANT: Howland, David S.
 ; APPLICANT: Marquis, Karen L.
 ; APPLICANT: Rosenzweig, Lipson, Sharon
 ; APPLICANT: Cockett, Mark Ian
 ; TITLE OF INVENTION: Transgenic Rat
 ; FILE REFERENCE: 3657/11046052
 ; CURRENT APPLICATION NUMBER: US/10/258,561
 ; 2001
 ; CURRENT FILING DATE: 2002-10-24
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: mouse G alpha 9 containing Gly to Ser substitution at codon 18
 ; OTHER INFORMATION: as well as several other changes to include an EE epitope tag
 ; OTHER INFORMATION: mouse G alpha 9 containing Gly to Ser substitution at codon 18
 ; OTHER INFORMATION: as well as several other changes to include an EE epitope tag
 ; US-10-258-561-2

Query Match 99.1%; Score 1844; DB 6; Length 359;
 Best Local Similarity 98.9%; Pred. No. 1.4e-182; Mismatches 2; Indels 0; Gaps 0;
 Matches 355; Conservative

QY 1 MTLESIMACCLSEAKERARRINDEIERVRRDKDARRELKULLLGGESGKSTFIQMR 60
 Db 1 MTLESIMACCLSEAKERARRINDEIERVRRDKDARRELKULLLGGESGKSTFIQMR 60
 Qy 61 IHGSGYSDEDKRKGFTKLVQNFITAMQAMIRAMDTLKIPIYKEHNKAHAOLVREDEVKE 120
 Db 61 IHGSGYSDEDKRKGFTKLVQNFITAMQAMIRAMDTLKIPIYKEHNKAHAOLVREDEVKE 120
 Qy 121 VSAFENPVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180
 Db 121 VSAFENPVDAIKSLWNPQIQCYDRREYOLSDSTKYLYNDLDRYADPAVLPTQDVL 180
 Qy 181 RVVPPTGIEPFDLSQVIFRMDVGQCSRERRKWHCFCENVTSMFLVALSEYDQVL 240
 Db 181 RVVPPTGIEPFDLSQVIFRMDVGQCSRERRKWHCFCENVTSMFLVALSEYDQVL 240
 Qy 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDYFPEYDGPQR 300
 Db 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDYFPEYDGPQR 300
 Qy 301 DAOARETILKMDVLNPDSDKITYSHTCATDTENIRFVFAVKDITLQNLKEYNLV 359
 Db 301 DAOARETILKMDVLNPDSDKITYSHTCATDTENIRFVFAVKDITLQNLKEYNLV 359

Db 301 DAQAAREFTIKMFVLDLNPDSKITYSHFTCATDTENIRFVAAVDTIQLNLKEYNLV 359 ; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Stouch, Terry
; TITLE OF INVENTION: MOLECULES THAT MODULATE G(ALPHA)q ACTIVITY AND METHODS OF
; PCT-US3-02452-13
; Sequence 13, Application PC/TUS302452
; GENERAL INFORMATION:
; APPLICANT: Moore, Lisa
; APPLICANT: Kindt, Rachel
; APPLICANT: Kopczynski, Jenny
; APPLICANT: Doberstein, Stephen
; APPLICANT: Cockett, Mark
; APPLICANT: Ramanathan, Chandra
; APPLICANT: Lodge, Nicholas
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Stouch, Terry
; TITLE OF INVENTION: MOLECULES THAT MODULATE G(ALPHA)q ACTIVITY AND METHODS OF
; FILE REFERENCE: 5624-277-999
; CURRENT APPLICATION NUMBER: US 10/352,843
; CURRENT FILING DATE: 2003-01-27
; PRIORITY FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 13
; LENGTH: 353
; SEQ ID NO 13
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: G-protein of the invention
; PCT-US3-02452-13
; Query Match 97.7%; Score 1817; DB 1; Length 353;
; Best Local Similarity 99.2%; Pred. No. 8.4e-180;
; Matches 350; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
; Qy' 7 MACC1SEAAEARRINDETERHVRDKDRARRELKLILLGTGESKSTFIKQMR1IHGSG 66
; 1 MACC1SEAAEARRINDETERHVRDKDRARRELKLILLGTGESKSTFIKQMR1IHGSG 60
; Db 67 YSDEDKRGFTKLVQONIFTAMQAMTRAMDTLKIPIKYKHEHKAHQALVRENDVKAFAEN 126
; Qy 61 YSDEDKRGFTKLVQONIFTAMQAMTRAMDTLKIPIKYKHEHKAHQALVRENDVKAFAEN 120
; Db 127 PYVDAIKSLANDPGIOECYDPRREYOLPSDKTYYLNDLDRVADPAVLPTQODVLRVPT 186
; 121 PYVDAIKSLANDPGIOECYDPRREYOLPSDKTYYLNDLDRVADPAVLPTQODVLRVPT 180
; Db 187 TG1IYFPDQSVIYRMDVQGQSERRKWICFENVTSMFLYVALESDQVIVESDEN 246
; Qy 181 TG1IYFPDQSVIYRMDVQGQSERRKWICFENVTSMFLYVALESDQVIVESDEN 240
; Db 247 RMEESKALFRITIYPPWFQNSVILFLNKKDLLEEKIMYSHLVYFPEYDGPQDQAAR 306
; Qy 241 RMEESKALFRITIYPPWFQNSVILFLNKKDLLEEKIMYSHLVYFPEYDGPQDQAAR 300
; Db 307 EFLKMFVLDLNPDSKITYSHFTCATDTENIRFVAAVDTIQLNLKEYNLV 359
; Db 301 EFLKMFVLDLNPDSKITYSHFTCATDTENIRFVAAVDTIQLNLKEYNLV 353
; RESULT 10
; US-09-724-676-49632
; Sequence 49632, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 49632
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-676-49632
; Query Match 90.7%; Score 1687; DB 5; Length 387;
; Best Local Similarity 89.4%; Pred. No. 3e-166;
; Matches 321; Conservative 23; Mismatches 15; Indels 0; Gaps 0;
; Qy 1 MTLESIMACCLSEAAEARRINDETERHVRDKDRARRELKLILLGTGESKSTFIKQMR 60
; Db 1 MTLESIMACCLSEAAEARRINDETERHVRDKDRARRELKLILLGTGESKSTFIKQMR 60

RESULT 9
; US-10-352-843-13
; Sequence 13, Application US/10352843
; GENERAL INFORMATION:
; APPLICANT: Moore, Lisa
; APPLICANT: Kindt, Rachel
; APPLICANT: Kopczynski, Jenny
; APPLICANT: Doberstein, Stephen
; APPLICANT: Cockett, Mark
; APPLICANT: Ramanathan, Chandra
; APPLICANT: Lodge, Nicholas

QY 61 IHGSGYSDEDKRGFFKWKWQNTFTAMQAMIRAMDTLKIYKPKYEHKAQLYREVDEVER 120
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIORITY NUMBER: 60/241, 755
 ; PRIORITY FILING DATE: 2000-10-20
 ; PRIORITY APPLICATION NUMBER: 60/237, 768
 ; PRIORITY FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231, 498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 7853
 ; LENGTH: 351
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-7853

QY RESULT 11
 ; Query Match 89.1%; Score 1657; DB 5; Length 351;
 ; Best Local Similarity 89.7%; Pred. No. 3.3e-163; Mismatches 15; Indels 0; Gaps 0;
 ; Matches 315; Conservative 21; Mismatches 15; Indels 0; Gaps 0;
 ; US-09-724-676A-49632

QY ; Sequence 4963, Application US/09724676A
 ; GENERAL INFORMATION:
 ; APPLICANT: Compugen LTD
 ; TITLE OF INVENTION: Variants of alternative splicing
 ; FILE REFERENCE: 129181.4 Compugen
 ; CURRENT APPLICATION NUMBER: US/09/724, 676A
 ; CURRENT FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 97222
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 49632
 ; LENGTH: 387
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-724-676A-49632

QY Query Match 90.7%; Score 1687; DB 5; Length 387;
 ; Best Local Similarity 89.4%; Pred. No. 3e-166; Mismatches 15; Indels 0; Gaps 0;
 ; Matches 321; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

QY 1 WTLSMACCLSEEEAKARRNDEIERVVRDKRDRARRELKILLGIGESCKSTFIKOMR 60
 ; 1 WTLSMACCLSEEEAKARRNDEIERVVRDKRDRARRELKILLGIGESCKSTFIKOMR 60
 ; 1 WTLSMACCLSEEEAKARRNDEIERVVRDKRDRARRELKILLGIGESCKSTFIKOMR 60

QY 61 IHRGSGTSDEDKRGFTKLYQVQNTFTAMQAMIRAMDTLKIYKPKYEHKAQLYREVDEVER 120
 ; 61 IHRGSGTSDEDKRGFTKLYQVQNTFTAMQAMIRAMDTLKIYKPKYEHKAQLYREVDEVER 120
 ; 61 IHRGSGTSDEDKRGFTKLYQVQNTFTAMQAMIRAMDTLKIYKPKYEHKAQLYREVDEVER 120

QY 121 VSAFENPVDAIKSLWNPQGIOCYDRREYQQLSDSTKYLNDLDRADPAVPLPTQDQVL 180
 ; 121 VSAFENPVDAIKSLWNPQGIOCYDRREYQQLSDSTKYLNDLDRADPAVPLPTQDQVL 180
 ; 121 VSAFENPVDAIKSLWNPQGIOCYDRREYQQLSDSTKYLNDLDRADPAVPLPTQDQVL 180

QY 181 RYRVPVIGIEPPDQSVIFRWDVGQQRSERKWRKWHCFENTISMPLVSEYDQVL 240
 ; 181 RYRVPVIGIEPPDQSVIFRWDVGQQRSERKWRKWHCFENTISMPLVSEYDQVL 240
 ; 181 RYRVPVIGIEPPDQSVIFRWDVGQQRSERKWRKWHCFENTISMPLVSEYDQVL 240

QY 241 ESDNENRMEESKALFRITITYPWFQNSVILINKKDLEEKIMYSHLVDYFPEYDQQR 300
 ; 241 ESDNENRMEESKALFRITITYPWFQNSVILINKKDLEEKIMYSHLVDYFPEYDQQR 300
 ; 241 ESDNENRMEESKALFRITITYPWFQNSVILINKKDLEEKIMYSHLVDYFPEYDQQR 300

QY 301 DAQAREFPLKMFVLDNPSDKIYSHFTCATDENTRFVAAVKDTIQLNLKEYNLV 359
 ; 301 DAQAREFPLKMFVLDNPSDKIYSHFTCATDENTRFVAAVKDTIQLNLKEYNLV 359
 ; 301 DAQAREFPLKMFVLDNPSDKIYSHFTCATDENTRFVAAVKDTIQLNLKEYNLV 359

QY RESULT 12
 ; Query Match 82.5%; Score 1535; DB 6; Length 355;
 ; Best Local Similarity 82.1%; Pred. No. 1.5e-150; Mismatches 28; Indels 0; Gaps 0;
 ; Matches 288; Conservative 35; Mismatches 28; Indels 0; Gaps 0;
 ; US-09-949-016-7853

QY ; Sequence 7853, Application US/09949016
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

XX
PS Claim 22; Page 24-25; 34pp; German.

XX
PS The present invention relates to a method of identifying compounds which
CC are capable of modifying the activity of a signal transduction pathway
CC which is dependent upon a G-protein coupled receptor. These compounds may
CC include the novel G-proteins 6q14myr (shown here), 6q15myr, 6q14, 6qs5
CC and Galphai6.

XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 1860; DB 23; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.6e-176; Mismatches 0; Indels 0; Gaps 0;
Matches 359; Conservative 0; MisMatches 0;

QY 1 MTLESIMACCOLSEEAKARRINDETERHVRDKDRARREKLILLGTGESSGSKSPFIKMR 60
Db 61 IIHGGSYSDDEDKRGFTKLKVONITFAMQAMIRAMDTLKIPIKYEHNKAHAQLVREDEVK 120

QY 121 VSAFENPYDAIKSLWNDPGIQECYDRRREYQLSDTKYLNDLRVADPAVLPQDVL 180
121 VSAFENPYDAIKSLWNDPGIQECYDRRREYQLSDTKYLNDLRVADPAVLPQDVL 180

QY 181 RVRVPTGTIEYPEFDLQSVIFRMVYDGGQRSERKWHFENVISIMFLVALSEYDQVIL 240
Db 181 RVRVPTGTIEYPEFDLQSVIFRMVYDGGQRSERKWHFENVISIMFLVALSEYDQVIL 240

QY 241 ESDNENRMEESKALETRITTYPWFTONSSVTLFLNKDLLEEKIMYSHLVDYFPEYDGQR 300
241 ESDNENRMEESKALETRITTYPWFTONSSVTLFLNKDLLEEKIMYSHLVDYFPEYDGQR 300

QY 301 DAQAREFILKMFVLDLNPDSKITYSHFTCATDTENIREVFAAVKDTIQLNKEYNLV 359
301 DAQAREFILKMFVLDLNPDSKITYSHFTCATDTENIREVFAAVKDTIQLNKEYNLV 359

RESULT 2

ABG68610 ID ABG68610 standard; Protein: 359 AA.

XX
AC ABG68610;
XX
AC ABG68610;XX
DT 07-OCT-2002 (first entry)XX
DE Human G protein alpha sub-unit q family #2.XX
DE G_q protein; sensory signaling; chemoreceptor; tastant; olfactory;XX
DE Human G protein alpha sub-unit; q family; G alpha q.XX
OS Homo sapiens.XX
PN WO200236622-A2.XX
PD 10-MAY-2002.XX
PF 24-OCT-2001; 2001WO-US32619.XX
PR 30-OCT-2000; 2000US-243770P.XX
PA (SENO-) SENOMYX INC.XX
PI Yao Y, Xu H;XX
DR WPI; 2002-519234/55.XX
PS Disclosure; Fig 2; 32pp; English.

XX
PS The invention describes an isolated variant of a G_q protein, which
CC exhibits increased promiscuity relative to the corresponding G_q protein.
CC The variant is used to identify a compound that modulates sensory
CC signaling in sensory cells and to identify a compound that interacts
CC with the G_q variant protein. The G_q protein variant is useful for
CC analysing and discovering agonists or antagonists of chemoreceptors, such
CC as G protein coupled receptors involved in sensing of tastants,
CC olfactory or pheromones. This is the amino acid sequence of a G protein
CC alpha sub-unit q family (G alpha q) protein that can functionally couple
CC to sensory cell receptors such as taste GPCRs (G protein-coupled
CC receptors) and olfactory GPCRs in an overly promiscuous manner.

XX
SQ Sequence 359 AA;

Query Match 99.4%; Score 1849; DB 23; Length 359;
Best Local Similarity 99.4%; Pred. No. 4.4e-175; Mismatches 1; Indels 0; Gaps 0;
Matches 357; Conservative 1; MisMatches 1;

QY 1 MTLESIMACCOLSEEAKARRINDETERHVRDKDRARREKLILLGTGESSGSKSPFIKMR 60
Db 61 IIHGGSYSDDEDKRGFTKLKVONITFAMQAMIRAMDTLKIPIKYEHNKAHAQLVREDEVK 120

QY 121 VSAFENPYDAIKSLWNDPGIQECYDRRREYQLSDTKYLNDLRVADPAVLPQDVL 180
121 VSAFENPYDAIKSLWNDPGIQECYDRRREYQLSDTKYLNDLRVADPAVLPQDVL 180

QY 181 RVRVPTGTIEYPEFDLQSVIFRMVYDGGQRSERKWHFENVISIMFLVALSEYDQVIL 240
Db 181 RVRVPTGTIEYPEFDLQSVIFRMVYDGGQRSERKWHFENVISIMFLVALSEYDQVIL 240

QY 241 ESDNENRMEESKALETRITTYPWFTONSSVTLFLNKDLLEEKIMYSHLVDYFPEYDGQR 300
241 ESDNENRMEESKALETRITTYPWFTONSSVTLFLNKDLLEEKIMYSHLVDYFPEYDGQR 300

QY 301 DAQAREFILKMFVLDLNPDSKITYSHFTCATDTENIREVFAAVKDTIQLNKEYNLV 359
Db 301 DAQAREFILKMFVLDLNPDSKITYSHFTCATDTENIREVFAAVKDTIQLNKEYNLV 359

RESULT 3

ABG68584 ID ABG68584 standard; Protein: 359 AA.

XX
AC ABG68584;XX
DT 07-OCT-2002 (first entry)XX
DE Mouse G protein alpha sub-unit q family.XX
DE G_q protein; sensory signaling; chemoreceptor; tastant; olfactory;XX
DE Human G protein alpha sub-unit; q family; G alpha q.XX
OS Mus musculus.XX
PN WO200236622-A2.XX
PD 10-MAY-2002.XX
PF 24-OCT-2001; 2001WO-US32619.XX
PR 30-OCT-2000; 2000US-243770P.XX
PA (SENO-) SENOMYX INC.XX
PI Yao Y, Xu H;XX
DR WPI; 2002-519234/55.

XX
PS New G-alpha-q protein variants, useful for analyzing and discovering
PT agonists or antagonists of chemoreceptors, such as G protein coupled
PT receptors involved in sensing of tastants, olfactants or pheromones -

PT New G-alpha-q protein variants, useful for analyzing and discovering
 PT agonists or antagonists of chemoreceptors, such as G protein coupled
 PT receptors involved in sensing of tastants, olfactants or pheromones
 XX

PS Claim 13; Fig 1; 32pp; English.

CC The invention describes an isolated variant of a G_q protein, which
 CC exhibits increased promiscuity relative to the corresponding G_q protein.
 CC The variant is used to identify a compound that modulates sensory
 CC signaling in sensory cells and to identify a compound that interacts
 CC with the G_q variant protein. The G_q protein variant is useful for
 CC analysing and discovering agonists or antagonists of chemoreceptors, such
 CC as G protein coupled receptors involved in sensing of tastants, olfactants or pheromones. This is the amino acid sequence of a G protein
 CC alpha sub-unit q family (G alpha q) protein that can functionally couple
 CC to sensory cell receptors such as taste GPCR's (G protein-coupled
 CC receptors) and olfactory GPCR's in an overly promiscuous manner.

XX

CC Sequence 359 AA;

CC

Query Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Pred	No.	8	8e-175	Indels	0	Gaps	0
Qy 1 MTLESIMACCLSEEAKARRINDEIERHVRDKRDRARRELKLILLGGESEKGSKTFIKMR	99.2%	1846	23	359	Matches 356;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;					
Db 1 MTLESIMACCLSEEAKARRINDEIERHVRDKRDRARRELKLILLGGESEKGSKTFIKMR	99.2%	1846	23	359										
Qy 61 IIHGSGYSDKRFKTLVQNYQITTAQMAMIRAMDTLKIPIKYEHNAHQLVREVEK	99.2%	1846	23	359										
Db 61 IIHGSGYSDKRFKTLVQNYQITTAQMAMIRAMDTLKIPIKYEHNAHQLVREVEK	99.2%	1846	23	359										
Qy 121 VSAFENPYVDAIKSLWNDPGIQECYDRRREYQVLSPTSKYLNDDLRVADPAVLPTQDVL	99.2%	1846	23	359										
Db 121 VSAFENPYVDAIKSLWNDPGIQECYDRRREYQVLSPTSKYLNDDLRVADPAVLPTQDVL	99.2%	1846	23	359										
Qy 181 RVRVPTTGIEIYEPFDLQSVIFRMVWDVGQSRERRKWHCENVTSMFLVSEQDV	99.1%	1844	23	359										
Db 181 RVRVPTTGIEIYEPFDLQSVIFRMVWDVGQSRERRKWHCENVTSMFLVSEQDV	99.1%	1844	23	359										
Qy 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDLIKEKTMWHLVDFPEYDGFQ	99.1%	1844	23	359										
Db 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDLIKEKTMWHLVDFPEYDGFQ	99.1%	1844	23	359										
Qy 301 DAQAREFLIKMFVLDLNPDSKDKIYSHFTCATDTENIRFVFAVKDTIQLNLKEYNV	99.1%	1844	23	359										
Db 301 DAQAREFLIKMFVLDLNPDSKDKIYSHFTCATDTENIRFVFAVKDTIQLNLKEYNV	99.1%	1844	23	359										
RESULT 4														
ARG68598														
ID ARG68598														
XX														
AC ARG68598;														
XX														
DT 07-OCT-2002 (first entry)														
XX														
DE Human G protein alpha sub-unit q family #1.														
XX														
KW G _q protein; sensory signaling; chemoreceptor; tastant; olfactant; pheromone; G protein alpha sub-unit; q family; G alpha q.														
XX														
OS Homo sapiens.														
PN WO2002136622-A2.														
XX														
PD 10-MAY-2002.														
XX														
PF 24-OCT-2001; 2001WO-US32619.														
XX														
PR 30-OCT-2000; 2000US-243770P.														
XX														
OS Homo sapiens.														

RESULT 5

AY49127

ID AY49127 standard; Protein: 1276 AA.

XX

AC AY49127;

XX

DT 07-JAN-2000 (first entry)

XX

DE phCaR/JmGluR2*Gq15 fusion construct protein sequence.

XX

OS

KW G-protein fusion receptor; CAR: calcium receptor; Glur: head injury; metabotropic glutamate receptor; GABAR: chimeric receptor; stroke; gamma-aminobutyric acid receptor; allosteric modulator; antagonist; spinal cord injury; epilepsy; ischaemia; hypoglycemia; anoxia; Alzheimer's disease; hyperparathyroidism; osteoporosis; depression; cognitive disorder.

XX

Best Local Similarity	98.6%	pred.	No. 4	9e-172;	Matches
QY	1	WTLIESMACCLUSEEAKAARRNDEIEHVRDKRDRARRELKLILGTGESGKSTFIKMR	60		
Qy	1	1 1 1 1 1 : 1 1 1 1 1	60		
Db	1036	WTLIESMACCLUSEEAKAARRNDEIEHVRDKRDRARRELKLILGTGESGKSTFIKMR	1095		
Qy	61	IIHGS3SDEDRGFKLVQYQIFTQAMTRAMDILKIPKRYEHKAHQALYREVDVEK	120		
Qy	1096	IIHGS3SDEDRGFKLVQYQIFTQAMTRAMDILKIPKRYEHKAHQALYREVDVEK	1155		
Db	121	VSAFENYVDAIKSLWNPQFOCYRREYOLSDSTKYLNDLDRVADPAPLQPOQVL	180		
Qy	1156	VSAFENYVDAIKSLWNPQFOCYRREYOLSDSTKYLNDLDRVADPAPLQPOQVL	1215		
Qy	181	RVYRPPTGIEIYPFDLQSVIRMDGGQSRERRKHKHCFENVTSMFLVALSETDQVLV	240		
Qy	1216	RVYRPPTGIEIYPFDLQSVIRMDGGQSRERRKHKHCFENVTSMFLVALSETDQVLV	1275		
Db	241	ESDNEENMEESALFRITTYWQFQNSVILFLNKDLLEKIMSHLVDFPEVQPOR	300		
Qy	1276	ESDNEENMEESALFRITTYWQFQNSVILFLNKDLLEKIMSHLVDFPEVQPOR	1335		
Qy	301	DAQAAREFILKMFYDMLPDSKLYIYHFTCAATDENTIREVAAVKOTIOLNLKEYNL	358		
Db	1336	DAQAAREFILKMFYDMLPDSKLYIYHFTCAATDENTIREVAAVKOTIOLNLKEYNL	1393		
RESULT	8				
AA015095					
ID					
AA015095		standard; Protein: 1394 AA.			
XX					
AC					
AA015095;					
XX					
DT					
22-AUG-2002		(first. entry)			
XX					
DE					
Human pmGluR2-CCR4-G-alpha-q15 fusion construct protein.					
XX					
KW					
Human; G-protein fusion receptor; extracellular domain; transmembrane domain; intracellular domain; GαR; mGluR; GABABR; modulator identification.					
KW					
XX					
OS					
Chimeric - Homo sapiens.					
XX					
PN					
W0200229033-A2.					
XX					
PD					
11-APR-2002.					
XX					
PR					
03-OCT-2000; 2000US-0679664.					
XX					
PD					
11-APR-2002.					
XX					
PR					
03-OCT-2001; 2001WO-US31074.					
XX					
PA					
(NPSP-) NPS PHARM INC.					
XX					
PI					
Stormann T, Hammerland LG, Storjohann LL, Busby JG, Garrett JE;					
PI					
Simin RT;					
XX					
DR					
WPI; 2002-330170/36.					
XX					
PT					
Novel G-protein fusion receptor, useful for identifying modulators of CarR, mGluR and GABABR, comprises G protein joined to the intracellular domain of the receptor -					
PT					
Novel G-protein fusion receptor, useful for identifying modulators of CarR, mGluR and GABABR, comprises G protein joined to the intracellular domain of the receptor -					
CC					
The invention comprises G-protein fusion receptors - comprising extracellular, transmembrane and intracellular domains similar to CarR, mGluR or GABABR receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CarR, mGluR and GABABR for use in treating associated conditions. The present amino acid sequence was used in the production of the invention.					
CC					

XX	Sequence	1394 AA;	CC	The invention relates to G-protein fusion receptors (1) comprising:
SQ			CC	(1) in the N to C direction, extracellular (ECB), transmembrane (TM) and
			CC	intracellular (ICD) domains, each chosen independently from a CAR
Query Match	98.2%	Score 1827; DB 23; Length 1394;	CC	(calcium receptor); Glur (metabotropic glutamate receptor) and GABAR
Best Local Similarity	98.6%	Pred. No. 4.9e-172;	CC	(gamma-aminobutyric acid receptor); (2) an optional linker attached to
Matches	353; Conservative	2; Mismatches	CC	the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the
QY	1	MTLESIMACCLSEEAKARINDETERHYRDKDRARRELKLLGTEGGSKSTFIKMR	CC	linker. (1), and recombinant chimeric receptors (CR) without the GP
		: : : : : : : : :	CC	component, are used to assess function of the various domains and to
Db	1036	MTLESIMACCLSEEAKARINDETERHYRDKDRARRELKLLGTEGGSKSTFIKMR	CC	identify compounds (e.g. allosteric modulators or antagonists) that act
QY	61	IIHGSYSDDDKRGTKLKVQNTIAMQAMIRAMDTLKIPIKYENKAHQALYREVDEK	CC	on these domains. The modulators are potentially useful for treating or
		: : : : : : : : :	CC	preventing diseases associated with the receptors, e.g. stroke, head or
Db	1096	IIHGSYSDDDKRGTKLKVQNTIAMQAMIRAMDTLKIPIKYENKAHQALYREVDEK	CC	spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia,
QY	121	VSASENPYDAIKSLWNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive
		: : : : : : : : :	CC	disorders and depression. Nucleic acid (11) that encodes (1) is used:
Db	1156	VSASENPYDAIKSLWNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	(1) for recombinant production of corresponding proteins; and (2) to
QY	181	RVRVPTGTIEYPFDLQSVIFRMVYDGGQRSERKWKHENVISIMFLVSEYDQVLV	CC	produce cells used in screening for modulators. Use of CAR and mGluR
		: : : : : : : : :	CC	domains allows presentation of GABAR domains, to a binding agent, in a
Db	1216	RVRVPTGTIEYPFDLQSVIFRMVYDGGQRSERKWKHENVISIMFLVSEYDQVLV	CC	form more like the natural domain structure compared with use of
QY	241	ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLLEKIMYSHLYDPEYDGPOR	CC	incomplete receptors, lacking one or more domains. By shuffling different
		: : : : : : : : :	CC	domains, agents can be identified that affect particular domains of a
Db	1276	ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLLEKIMYSHLYDPEYDGPOR	CC	receptor.
QY	301	DAQAREFILKMFVDLNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	
Db	1336	DAQAREFILKMFVDLNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	
QY	RESULT 9	Query Match 98.2%; Score 1827; DB 20; Length 1397;	CC	
AY49134	ID AY49134	standard; Protein; 1397 AA.	CC	
XX	AC AY49134;		CC	
XX	DT 07-JAN-2000	(first entry)	CC	
DE	pmGluR2/GaR*Galphai3+3Ala linker fusion construct protein sequence.		CC	
XX			CC	
QY	61	IIHGSYSDDDKRGTKLKVQNTIAMQAMIRAMDTLKIPIKYENKAHQALYREVDEK	CC	
Db	1099	IIHGSYSDDDKRGTKLKVQNTIAMQAMIRAMDTLKIPIKYENKAHQALYREVDEK	CC	
QY	121	VSASENPYDAIKSLWNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	
Db	1039	MTLESIMACCLSEEAKARINDETERHYRDKDRARRELKLLGTEGGSKSTFIKMR	CC	
QY	181	RVRVPTGTIEYPFDLQSVIFRMVYDGGQRSERKWKHENVISIMFLVSEYDQVLV	CC	
Db	1159	VSASENPYDAIKSLWNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	
QY	1219	RVRVPTGTIEYPFDLQSVIFRMVYDGGQRSERKWKHENVISIMFLVSEYDQVLV	CC	
Db	1219	RVRVPTGTIEYPFDLQSVIFRMVYDGGQRSERKWKHENVISIMFLVSEYDQVLV	CC	
QY	241	ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLLEKIMYSHLYDPEYDGPOR	CC	
Db	1279	ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLLEKIMYSHLYDPEYDGPOR	CC	
QY	301	DAQAREFILKMFVDLNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	
Db	1339	DAQAREFILKMFVDLNPDSKIIYSHFTQATDENTIREVFAAVKDTIQLQNLKEYNL	CC	
QY	RESULT 10	Query Match 98.2%; Score 1827; DB 20; Length 1397;	CC	
AA015100	ID AA015100	standard; Protein; 1397 AA.	CC	
XX	AC AA015100;		CC	
PR	DT 22-AUG-2002	(first entry)	CC	
PA			CC	
(NPSP-)	NPS PHARM INC.		CC	
XX	PI Stommann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JE;		CC	
XX	Simin RT;		CC	
DR	WPI; 1999-610995/52.		CC	
N-PSDB	DAZ31065.		CC	
XX	New G-protein fusion receptors and chimeras containing domains from		CC	
PT	different receptors, used to screen for modulators, potentially useful		CC	
PT	e.g. for treating or preventing stroke or Alzheimer's disease		CC	
XX			CC	
PS	Example 1; Fig 12; 255pp; English.		CC	
XX	W0200229033-A2.		CC	
XX	PD 11-APR-2002.		CC	

XX 03-OCT-2001; 2001WO-US31074. .
 PF PN WO200229033-A2.
 XX XX
 PR 03-OCT-2000; 2000US-0679664..
 XX XX
 PA (NPSP-) NPS PHARM INC.
 XX PI Stormann T, Hammerland LG, Storjohann LL, Busby JG, Garrett JE;
 PI Simin RT;
 XX XX
 DR WPI; 2002-330170/36.
 XX
 PS Disclosure: Fig 12; 168pp; English.
 XX
 CC The invention comprises G-protein fusion receptors - comprising
 CC extracellular, transmembrane and intracellular domains similar to CAR,
 CC mGluR or GABAB receptor sequences. The G-protein fusion receptors of the
 CC invention may also possess a linker joined to the carboxy terminus of the
 CC intracellular domain, and a G-protein joined to the linker. The G-protein
 CC fusion receptors of the invention are useful for identifying modulators
 CC of CAR, mGluR and GABAB for use in treating associated conditions. The
 CC present amino acid sequence was used in the production of the invention.
 SQ Sequence 1397 AA;
 Query Match 98.2%; Score 1827; DB 23; Length 1397;
 Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MTLESIMACCLSBEEKARRINDEIERVVRDKRDRRELKILLGGESEKSTFKQMR 60
 Db 1039 MTLESIMACCLSBEEKARRINDEIERVVRDKRDRRELKILLGGESEKSTFKQMR 1098
 QY 61 IHGSGSYSDEDKRGFTKLVQNIFTAMQAMIRAMDTLKIPIKYEHNAQALVREYDEK 120
 Db 1099 IHGSGSYSDEDKRGFTKLVQNIFTAMQAMIRAMDTLKIPIKYEHNAQALVREYDEK 1158
 QY 121 VSAFENIVYDAIKSLWNPDGTQECYDRREYQYLDSDSTKYYLNDLDRVADPAVLPTQODVL 180
 Db 1159 VSAFENIVYDAIKSLWNPDGTQECYDRREYQYLDSDSTKYYLNDLDRVADPAVLPTQODVL 1218
 QY 181 RVVPTGQIEVPFDLQSVIFRMDVGQQRSERKWHCFENVTSMFLVALSEYDQVL 240
 Db 1219 RVVPTGQIEVPFDLQSVIFRMDVGQQRSERKWHCFENVTSMFLVALSEYDQVL 1278
 QY 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDFFPEYDGQR 300
 Db 1279 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDFFPEYDGQR 1338
 QY 301 DAQAREFILKMEVDLNPDSKTIYSHTCATDTENIRFVFAVKDITLQNLKDCGL 358
 Db 1339 DAQAREFILKMEVDLNPDSKTIYSHTCATDTENIRFVFAVKDITLQNLKDCGL 1396
 RESULT 11
 AAO15105 ID AAO15105 standard; Protein: 1402 AA.
 AC AAO15105;
 XX
 DT 22-AUG-2002 (first entry)
 DE Human Ph2SPMgluR3-Car*AAA*Gq15 fusion construct protein sequence.
 KW Human; G-protein fusion receptor; extracellular domain;
 KW transmembrane domain; intracellular domain; CAR; mGluR; GABAB;
 KW modulator identification.
 XX Chimeric - Homo sapiens.
 OS

XX 03-OCT-2001; 2001WO-US31074. .
 PF PN WO200229033-A2.
 XX XX
 PD 11-APR-2002.
 XX XX
 PR 03-OCT-2000; 2000US-0679664.
 XX XX
 PA (NPSP-) NPS PHARM INC.
 XX PI Stormann T, Hammerland LG, Storjohann LL, Busby JG, Garrett JE;
 PI Simin RT;
 XX XX
 DR WPI; 2002-330170/36.
 XX
 PS Disclosure: Fig 18; 168pp; English.
 XX
 CC The invention comprises G-protein fusion receptors - comprising
 CC extracellular, transmembrane and intracellular domains similar to CAR,
 CC mGluR or GABAB receptor sequences. The G-protein fusion receptors of the
 CC invention may also possess a linker joined to the carboxy terminus of the
 CC intracellular domain, and a G-protein joined to the linker. The G-protein
 CC fusion receptors of the invention are useful for identifying modulators
 CC of CAR, mGluR and GABAB for use in treating associated conditions. The
 CC present amino acid sequence was used in the production of the invention.
 SQ Sequence 1402 AA;
 Query Match 98.2%; Score 1827; DB 23; Length 1402;
 Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MTLESIMACCLSBEEKARRINDEIERVVRDKRDRRELKILLGGESEKSTFKQMR 60
 Db 1044 MTLESIMACCLSBEEKARRINDEIERVVRDKRDRRELKILLGGESEKSTFKQMR 1103
 QY 61 IHGSGSYSDEDKRGFTKLVQNIFTAMQAMIRAMDTLKIPIKYEHNAQALVREYDEK 120
 Db 1104 IHGSGSYSDEDKRGFTKLVQNIFTAMQAMIRAMDTLKIPIKYEHNAQALVREYDEK 1163
 QY 121 VSAFENIVYDAIKSLWNPDGTQECYDRREYQYLDSDSTKYYLNDLDRVADPAVLPTQODVL 180
 Db 1164 VSAFENIVYDAIKSLWNPDGTQECYDRREYQYLDSDSTKYYLNDLDRVADPAVLPTQODVL 1223
 QY 181 RVVPTGQIEVPFDLQSVIFRMDVGQQRSERKWHCFENVTSMFLVALSEYDQVL 240
 Db 1224 RVVPTGQIEVPFDLQSVIFRMDVGQQRSERKWHCFENVTSMFLVALSEYDQVL 1283
 QY 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDFFPEYDGQR 300
 Db 1284 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDOLLEEKIMYSHLVDFFPEYDGQR 1343
 QY 301 DAQAREFILKMEVDLNPDSKTIYSHTCATDTENIRFVFAVKDITLQNLKDCGL 358
 Db 1344 DAQAREFILKMEVDLNPDSKTIYSHTCATDTENIRFVFAVKDITLQNLKDCGL 1401
 RESULT 12
 AAY49131 ID AAY49131 standard; Protein: 1418 AA.
 AC AAY49131;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE mGluR3/Car*Galphaq15 fusion construct protein sequence.

Db	1240	RVRVPPTGILIEYPFEDQSVIFRMVYGGQRSERRKWIKHPEVNTSIMFLVALSEYDQVLV	1299
KW	G-protein fusion receptor; CAR; calcium receptor; Glur; head injury;		
KW	metabotropic glutamate receptor; GABAR; chimeric receptor; stroke;		
KW	gamma-aminobutyric acid receptor; allosteric modulator; antagonist;		
KW	spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia;		
KW	Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;		
KW	cognitive disorder.		
XX	Homo sapiens.		
OS			
XX			
PN	W0951641-A1.		
XX			
PD	14-OCT-1999.		
XX			
PF	02-APR-1999;	99WO-US07333.	
XX			
PR	03-APR-1998;	98US-0080671.	
XX			
PA	(NPSP-) NPS PHARM INC.		
XX			
PI	Stormann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JE;		
PT	Simin RT;		
XX			
DR	WPI; 1998-610995/52.		
DR	N-PSDB; AAZ31062.		
XX			
PT	New G-protein fusion receptors and chimeras containing domains from		
PT	different receptors, used to screen for modulators, potentially useful		
PT	e.g. for treating or preventing stroke or Alzheimer's disease		
XX			
PS	Example 1; Fig 12; 25pp; English.		
XX			
CC	The invention relates to G-protein fusion receptors (I) comprising:		
CC	(1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and		
CC	intracellular (ICD) domains, each chosen independently from a CAR		
CC	calcium receptor), Glur (metabotropic glutamate receptor) and GABAR		
CC	(gamma-aminobutyric acid receptor); (2) an optional linker attached to		
CC	the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the		
CC	linker. (I), and recombinant chimeric receptors (CR) without the GP		
CC	component, are used to assess function of the various domains and to		
CC	identify compounds (e.g. allosteric modulators or antagonists) that act		
CC	on these domains. The modulators are potentially useful for treating or		
CC	preventing diseases associated with the receptors, e.g. stroke, head or		
CC	spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia,		
CC	Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive		
CC	disorders and depression. Nucleic acid (II) that encodes (I) is used:		
CC	(1) for recombinant production of corresponding proteins; and (2) to		
CC	produce cells used in screening for modulators. Use of CAR and mGlur		
CC	domains allows presentation of GABAR domains, to a binding agent, in a		
CC	form more like the natural domain structure compared with use of		
CC	incomplete receptors, lacking one or more domains. By shuffling different		
CC	domains, agents can be identified that affect particular domains of a		
CC	receptor.		
XX			
SQ	Sequence 1418 AA;		
	Query Match 98.2%; Score 1827; DB 20; Length 1418;		
	Best Local Similarity 98.6%; Pred. No. 5e-172; 3; Indels 0; Gaps 0;		
	Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Qy	1 MTLESIMACCLSEEAKARRINDETERHYRDKDARRELKLILLGIGESGKSFPIKOMR 60		
Db	1060 MTLESIMACCLSEEAKARRINDETERHYRDKDARRELKLILLGIGESGKSFPIKOMR 1119		
Qy	61 IIHSGSYSDDKRGFTKLVYQNTIAMPAMIRAMDTLKIPIKYEHNKAHQLYREVDEK 120		
Db	1120 IIHSGSYSDDKRGFTKLVYQNTIAMPAMIRAMDTLKIPIKYEHNKAHQLYREVDEK 1179		
Qy	121 VSAFENPYDAIKSLWNDPGIQCEDYRREYQSLDSTKYLNDLDRVPAYLPTQDVL 180		
Db	1180 VSAFENPYDAIKSLWNDPGIQCEDYRREYQSLDSTKYLNDLDRVPAYLPTQDVL 1239		
Qy	181 RVRPTTGIEIYPLDQSYTFRMVDVGGQRSERKWIKEFENYVSIMFLWSEYDQVL 240		
XX			
SQ	Sequence 1418 AA;		
	Query Match 98.2%; Score 1827; DB 23; Length 1418;		
	Best Local Similarity 98.6%; Pred. No. 5e-172; 3; Indels 0; Gaps 0;		
	Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Qy	1 MTLESIMACCLSEEAKARRINDETERHYRDKDARRELKLILLGIGESGKSFPIKOMR 60		
Db	1060 MTLESIMACCLSEEAKARRINDETERHYRDKDARRELKLILLGIGESGKSFPIKOMR 1119		
Qy	61 IIHSGSYSDDKRGFTKLVYQNTIAMPAMIRAMDTLKIPIKYEHNKAHQLYREVDEK 120		
Db	1120 IIHSGSYSDDKRGFTKLVYQNTIAMPAMIRAMDTLKIPIKYEHNKAHQLYREVDEK 1179		
Qy	121 VSAFENPYDAIKSLWNDPGIQCEDYRREYQSLDSTKYLNDLDRVPAYLPTQDVL 180		

Db 1064 MTLSEMACCLSEEAKEARRINDETERQLRRDKRDRRELKLLLTGEGSKSTFKOMR 1123
Qy 61 IIHGSYSDDEKRGFKLKVQNIFTAMQAMIRAMDTIKIPYKYEHNKAHQLVREVDVEK 120
Db 1124 IIHGSYSDDEKRGFKLKVQNIFTAMQAMIRAMDTIKIPYKYEHNKAHQLVREVDVEK 1183
Qy 121 VSAFENYVDAIKSLWMDPGIQECYDREYQQLSDSTKYLNDLDRVADAYLPTQODVL 1243
Db 1184 VSAFENPVIDAIKSLWMDPGIQECYDREYQQLSDSTKYLNDLDRVADAYLPTQODVL 1243
Qy 181 RVRVPPTGILITYPFDIQLQSVTRMVDYGGOSERRKVTICFENUTSMELLAELSEYDQVW 240
Db 1244 RVRVPPTGILITYPFDIQLQSVTRMVDYGGOSERRKVTICFENUTSMFLAELSEYDQVW 1303
Qy 241 ESDNEURMEESKALFRITITYPWFQNSVUFLNKDLLEEKIMSHLVYFPEFDGPOR 300
Db 1304 ESDNEURMEESKALFRITITYPWFQNSVUFLNKDLLEEKIMSHLVYFPEFDGPOR 1363
Qy 301 DAQAAREFLKMEVDLAPDSRKLISHFTICATDTEIRFWFAAVKDTIQLNLKTYNL 358
Db 1364 DAQAAREFLKMEVDLAPDSRKLISHFTICATDTEIRFWFAAVKDTIQLNLKDOGL 1421

Search completed: June 30, 2003, 16:16:16
Job time : 45 secs

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GenCore Version 5.1.6

Run on: June 30, 2003, 16:15:31 ; Search time 15 seconds

Perfect score: 1860

Sequence: MTLESIMACCLSEEKAREARR... VFAAVKDTIQLQNLKEYNLV 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/9CTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1056	57.3	374	US-03-878-801-4
2	1063	57.2	374	US-09-442-349A-29
3	1063	57.2	374	US-03-442-349A-31
4	1062	57.1	374	US-03-442-349A-21
5	1062	57.1	374	US-09-442-349A-29
6	1062	57.1	374	US-03-442-349A-25
7	1062	57.1	374	US-03-442-349A-30
8	1062	57.1	374	US-09-442-349A-32
9	1062	57.1	374	US-03-442-349A-34
10	1061	57.0	374	US-03-442-349A-2
11	1061	57.0	374	US-09-442-349A-22
12	1061	57.0	374	US-03-442-349A-24
13	1061	57.0	374	US-03-442-349A-33
14	1058	56.9	374	US-03-442-349A-26
15	1058	56.9	374	US-03-442-349A-28
16	1057	56.8	374	US-09-442-349A-20
17	1057	56.8	374	US-09-442-349A-27
18	1055	56.7	374	US-03-18-442-349-2
19	1054	56.7	374	US-03-442-349A-14
20	1054	56.7	374	US-09-442-349A-16
21	1053	56.6	365	US-03-442-349A-108
22	1053	56.6	374	US-09-442-349A-6
23	1053	56.6	374	US-09-442-349A-8
24	1053	56.6	374	US-03-442-349A-10
25	1053	56.6	374	US-03-442-349A-15
26	1053	56.6	374	US-09-442-349A-17
27	1053	56.6	374	US-09-442-349A-19

ALIGNMENTS

RESULT 1	US-08-878-801-4
SEQUENCE 4, Application	SEQUENCE 4, Appli
PATENT NO. 6004808	
GENERAL INFORMATION:	
APPLICANT: Negulescu, Paul	
APPLICANT: Offermanns, Stefan	
APPLICANT: Zuker, Charles	
TITLE OF INVENTION: PROMISCUOUS G-PROTEINS COMPOSITIONS AND THEIR USE	
FILE REFERENCE: 0836602001	
CURRENT APPLICATION NUMBER: US-08-878,801	
CURRENT FILING DATE: 1997-06-19	
EARLIER APPLICATION NUMBER: US 60-020,234	
EARLIER FILING DATE: 1996-06-21	
NUMBER OF SEQ ID NOS: 4	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 4	
LENGTH: 374	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-08-878-801-4	
QUERY MATCH	57.3%; Score 1056; DB 3; Length 374;
BEST LOCAL SIMILARITY	57.2%; Pred. No. 7.7e-100;
MATCHES	207; Conservative 55; Mismatches 88; Indels 12; Gaps 2;
SEQUENCE 21, APPLI	
SEQUENCE 23, APPLI	
SEQUENCE 25, APPLI	
SEQUENCE 30, APPLI	
SEQUENCE 32, APPLI	
SEQUENCE 34, APPLI	
SEQUENCE 2, APPLI	
SEQUENCE 22, APPLI	
SEQUENCE 24, APPLI	
SEQUENCE 33, APPLI	
SEQUENCE 26, APPLI	
SEQUENCE 28, APPLI	
SEQUENCE 20, APPLI	
SEQUENCE 27, APPLI	
SEQUENCE 2, APPLI	
SEQUENCE 14, APPLI	
SEQUENCE 16, APPLI	
SEQUENCE 108, APPLI	
SEQUENCE 6, APPLI	
SEQUENCE 8, APPLI	
SEQUENCE 10, APPLI	
SEQUENCE 15, APPLI	
SEQUENCE 17, APPLI	
SEQUENCE 19, APPLI	
DB	
QY	
10	CLESEAREKARRINDEIERHVRDKRDRARRELKLILLGIGESGKSTFIKOMRITHGSGSD 69
11	: - : : : :
12	13 CTEEEKTAARIQDIBINRILLEOKKORESELKILLLGPGESKSTFIKOMRITHGVGSE 72
13	: - :
14	70 EDKRGFTKLVYQNLITAMQAMIRAMDTLKIPTYKEHNKAHQALVREVDVERKAFENPV 129
15	: - :
16	73 EDERRAFRLLIQYNTIVSQMAMIDRQLQIPPSRPSDKOHALSTMQTDPYKVSTFEKPA 132
17	: - :
18	130 DAIKSLWNPGIQCEDYDRREYQLSDSTKYLNDLDRDPAVYIPTQDYLRYRPTG 189
19	: - :
20	133 VAMQJLWDRAGIRACAYERREFHLLSDAYVLSHLERISDESDYPTAQDYLRSMPTE 192
21	: - :
22	190 IYYPDLQSVIFRMWDVGGORSERRKWHCPFNNTSIMLVALEYDQVLVSEDNRME 249
23	: - :
24	193 NEYCYSVKKRKLIVDGGCRSRKWKHCNFVNITYLTLASLSEYDQCLEENDQENR 252
25	: - :
26	250 ESKALFRTILTYPWQFQNSVTLFLNKDLIEEKIMYSHLVDYFPEYDQFQDQAARET 309
27	: - :
28	253 ESLALFSTILELPWPKTSIVFLNLKTDIEKDHTSHATYFPEQGPRRDAAKSF 312
29	: - :
30	310 LKMFYDLD----NPSPD-----KLYHHTCATDTEIMRFVPAVKOTIQLQNLKE 357
31	: - :
32	313 LDMDVRYVVASCAEPDGGRKGSRARFFCACTDOSVRSKVRDVRVSLARYLDE 372

QY 130 DAIKSLANDPGCIOECYDERRREYQLSDSLTKYLNLDRAVDAVLPTQDVLVRVPTGI 189
 Db 133 AAMQWLRWDAGIRACYERRREFHLLSDAVYLSHLERITEEGVPTAODVLSRMRPTGI 192
 QY 190 IEPFDIQLOSVIRFMVYDVGQGORSERRKWHCFENVTISMLVASEDQVIVESDNENRME 249
 Db 193 NEYCFSVOKTNLRIVDVGQGOKSERRKWHCFENVTISMLVASEDQVIVESDNENRME 252
 QY 250 ESKALERTITYPWFQNSVILFLNKDLEEKIMSHLVDYFPEPDGQDQAAREFI 309
 Db 253 ESLALFGTILELWFKSTSVILFLNKTDILEEKIPSHLATEFPEFQGPKDAEAKRFI 312
 QY 310 LKMFVDL-----NPDS-----KITYSHFTCATDENIRFVAVKDTIQLQNLKEYN 357
 Db 313 LDMDYRMTGCVDGPPEGSNRNRKETKEIYSHFTCATDTNSNQFVQAVTDVIIQNLKYIG 372
 QY 358 L 358
 Db 373 L 373

RESULT 5
 US-09-442-349A-23
 ; Sequence 23, Application US/09442349A
 ; Patent No. 6463178
 ; GENERAL INFORMATION:
 ; APPLICANT: Wong, Yung H
 ; TITLE OF INVENTION: G Protein
 ; FILE REFERENCE: M99/0101/US
 ; CURRENT APPLICATION NUMBER: US/09/442, 349A
 ; CURRENT FILING DATE: 1999-11-17
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 25
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: G protein
 ; OTHER INFORMATION: US-09-442-349A-23

Query Match 57.1%; Score 1062; DB 4; Length 374.
 Best Local Similarity 57.1%; Pred. No. 2e-99; Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;
 Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;

QY 10 CLESEEAEARRNDETERHYRDKRDRARRELKILLGCGESGSTFIKOMRITHGSGYSD 69
 Db 13 CLTDEDEKAARVQDQEINRILLEQOKDRGELKLILLGPGESGKSTFIKOMRITHGAGYE 72
 QY 70 EDKRGFTKLVQNFAMQAMIRAMDTLKFYKPYKHNKAHQLVREVDVEKVSAFENPV 129
 Db 73 EERKFRPPLYVIVFVSMRAMELORLQFSPRSPEKHSRSLVMSQDVKYVTEKRYA 132
 QY 130 DAIKSLANDPGCIOECYDERRREYQLSDSLTKYLNLDRAVDAVLPTQDVLVRVPTGI 189
 Db 133 AAMQWLRWDAGIRACYERRREFHLLSDAVYLSHLERITEEGVPTAODVLSRMRPTGI 192
 QY 190 IEPFDIQLOSVIRFMVYDVGQGORSERRKWHCFENVTISMLVASEDQVIVESDNENRME 249
 Db 193 NEYCFSVOKTNLRIVDVGQGOKSERRKWHCFENVTISMLVASEDQVIVESDNENRME 252
 QY 250 ESKALERTITYPWFQNSVILFLNKDLEEKIMSHLVDYFPEPDGQDQAAREFI 309
 Db 253 ESLALFGTILELWFKSTSVILFLNKTDILEEKIPSHLATEFPEFQGPKDAEAKRFI 312
 QY 310 LKMFVDL-----NPDS-----KITYSHFTCATDENIRFVAVKDTIQLQNLKEYN 357
 Db 313 LDMDYRMTGCVDGPPEGSNRNRKETKEIYSHFTCATDTNSNQFVQAVTDVIIQNLKYIG 372
 QY 358 L 358
 Db 373 L 373

RESULT 6
 US-09-442-349A-25
 ; Sequence 30, Application US/09442349A
 ; Patent No. 6462178
 ; GENERAL INFORMATION:
 ; APPLICANT: Wong, Yung H
 ; TITLE OF INVENTION: G Protein
 ; FILE REFERENCE: M99/0101/US
 ; CURRENT APPLICATION NUMBER: US/09/442, 349A
 ; CURRENT FILING DATE: 1999-11-17
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 25
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: G protein
 ; OTHER INFORMATION: US-09-442-349A-25

Query Match 57.1%; Score 1062; DB 4; Length 374.
 Best Local Similarity 57.1%; Pred. No. 2e-99; Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;
 Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;

QY 10 CLESEEAEARRNDETERHYRDKRDRARRELKILLGCGESGSTFIKOMRITHGSGYSD 69
 Db 13 CLTDEDEKAARVQDQEINRILLEQOKDRGELKLILLGPGESGKSTFIKOMRITHGAGYE 72
 QY 70 EDKRGFTKLVQNFAMQAMIRAMDTLKFYKPYKHNKAHQLVREVDVEKVSAFENPV 129
 Db 73 EERKFRPPLYVIVFVSMRAMELORLQFSPRSPEKHSRSLVMSQDVKYVTEKRYA 132
 QY 130 DAIKSLANDPGCIOECYDERRREYQLSDSLTKYLNLDRAVDAVLPTQDVLVRVPTGI 189
 Db 133 AAMQWLRWDAGIRACYERRREFHLLSDAVYLSHLERITEEGVPTAODVLSRMRPTGI 192
 QY 190 IEPFDIQLOSVIRFMVYDVGQGORSERRKWHCFENVTISMLVASEDQVIVESDNENRME 249
 Db 193 NEYCFSVOKTNLRIVDVGQGOKSERRKWHCFENVTISMLVASEDQVIVESDNENRME 252
 QY 250 ESKALERTITYPWFQNSVILFLNKDLEEKIMSHLVDYFPEPDGQDQAAREFI 309
 Db 253 ESLALFGTILELWFKSTSVILFLNKTDILEEKIPSHLATEFPEFQGPKDAEAKRFI 312
 QY 310 LKMFVDL-----NPDS-----KITYSHFTCATDENIRFVAVKDTIQLQNLKEYN 357
 Db 313 LDMDYRMTGCVDGPPEGSNRNRKETKEIYSHFTCATDTNSNQFVQAVTDVIIQNLKYIG 372
 QY 358 L 358
 Db 373 L 373

RESULT 7
 US-09-442-349A-30
 ; Sequence 30, Application US/09442349A
 ; Patent No. 6462178
 ; GENERAL INFORMATION:
 ; APPLICANT: Wong, Yung H
 ; TITLE OF INVENTION: G Protein
 ; FILE REFERENCE: M99/0101/US
 ; CURRENT APPLICATION NUMBER: US/09/442, 349A
 ; CURRENT FILING DATE: 1999-11-17
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 30
 ; LENGTH: 374
 ; TYPE: PRT
 ; OTHER INFORMATION: Description of Artificial Sequence: G protein
 ; OTHER INFORMATION: US-09-442-349A-30

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: chimera

US-09-442-349A-30

Query Match Best Local Similarity 57.1%; Score 1062; DB 4; Length 374; Matches 206; Conservative 57; Mismatches 86; Indels 12; Gaps 2;

Best Local Similarity 57.1%; Score 1062; DB 4; Length 374; Matches 206; Conservative 57; Mismatches 86; Indels 12; Gaps 2;

QY 10 CLESEEKAARINDEIERHVRDRKDRARRELKLILLGGESEKGKSTFIKOMRITHGSGSD 69
Db 13 CLTDEKAARVDOEINRILLEQKQDRGELKLILLGPGESGRKSTFIKOMRITHGAGYE 72

QY 70 EDKRGFTKLYQNTAMQAMIRAMDTLKIPYKVBHKAHQRLVREVDYEVKSAFENPVY 129
Db 73 EERKGFRPLVQNTFVSMRAMEAMERLQIPFSRPSKHSVMSDQPKVTFKRYA 132

QY 130 DAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVLVRVPTGI 189
Db 133 AAMQWLWRDAGIRACYERRFHLLDSAVVYLSHLERITEEGYVPTAQVQLRSRMPPTGI 192

QY 190 IEPFDLQSVIFRMVDDGGORSERRKWIFHENVTSMFLVALSEYDQVLESDNRM 249
Db 193 NEYCPSVQKLNRLTVYDVGOKSERRKWIFHENVTSMFLVALSEYDQVLEENQENRM 252

QY 250 ESKAFLRTITYPWNQNSVILFLNKDLEEKTMVSHADYFPEYDGFORDQAAREFI 309
Db 253 ESLALFTILELPWFKSTSVLFLNKTDLIEKIPTSHLATYFSPSFQGRQDAAKRFI 312

QY 310 LKMFVDL-----NPDSD-----KITYSHTCATDENTIREVAAVKOTIQLNKEYN 357
Db 313 LDMDTRMTGCVGDGPEGSNRNKEKTYIYSHFTCATDNNIOPFVFEAVTDVIONNLKYIG 372

QY 358 L 358
Db 373 L 373

RESULT 9
US-09-442-349A-34
; Sequence 34, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: chimera

US-09-442-349A-34

Query Match Best Local Similarity 57.1%; Score 1062; DB 4; Length 374; Matches 206; Conservative 57; Mismatches 86; Indels 12; Gaps 2;

Best Local Similarity 57.1%; Score 1062; DB 4; Length 374; Matches 206; Conservative 57; Mismatches 86; Indels 12; Gaps 2;

QY 10 CLESEEKAARINDEIERHVRDRKDRARRELKLILLGGESEKGKSTFIKOMRITHGSGSD 69
Db 13 CLTDEKAARVDOEINRILLEQKQDRGELKLILLGPGESGRKSTFIKOMRITHGAGYE 72

QY 70 EDKRGFTKLYQNTAMQAMIRAMDTLKIPYKVBHKAHQRLVREVDYEVKSAFENPVY 129
Db 73 EERKGFRPLVQNTFVSMRAMEAMERLQIPFSRPSKHSVMSDQPKVTFKRYA 132

QY 130 DAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVLVRVPTGI 189
Db 133 AAMQWLWRDAGIRACYERRFHLLDSAVVYLSHLERITEEGYVPTAQVQLRSRMPPTGI 192

QY 190 IEPFDLQSVIFRMVDDGGORSERRKWIFHENVTSMFLVALSEYDQVLESDNRM 249
Db 193 NEYCPSVQKLNRLTVYDVGOKSERRKWIFHENVTSMFLVALSEYDQVLEENQENRM 252

QY 250 ESKAFLRTITYPWNQNSVILFLNKDLEEKTMVSHADYFPEYDGFORDQAAREFI 309
Db 253 ESLALFTILELPWFKSTSVLFLNKTDLIEKIPTSHLATYFSPSFQGRQDAAKRFI 312

QY 310 LKMFVDL-----NPDSD-----KITYSHTCATDENTIREVAAVKOTIQLNKEYN 357
Db 313 LDMDTRMTGCVGDGPEGSNRNKEKTYIYSHFTCATDNNIOPFVFEAVTDVIONNLKYIG 372

QY 358 L 358
Db 373 L 373

US-09-442-349A-22

Query Match 57.0%; Score 1061; DB 4; Length 374;
Best Local Similarity 57.1%; Pred. No. 2.5e-99;
Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;

GENERAL INFORMATION:
APPLICANT: Wong, Yung H
TITLE OF INVENTION: G Protein
FILE REFERENCE: M9/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 374

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: G protein
OTHER INFORMATION: chimera
US-09-442-349A-2

Query Match 57.0%; Score 1061; DB 4; Length 374;
Best Local Similarity 57.1%; Pred. No. 2.5e-99;
Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;

GENERAL INFORMATION:
APPLICANT: Wong, Yung H
TITLE OF INVENTION: G Protein
FILE REFERENCE: M9/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 374

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: G protein
OTHER INFORMATION: chimera

Qy 10 C1SEEKEARINDEERHVRDKRDRARREKLILLGTEGESSKSTFKOMRITHGSGSD 69
Db 13 C1TEDEKAARVQDQEINRILLFQKQDRGEKLILLGPGESSKSTFKOMRITHGAGYE 72
Qy 70 EDRKRGFTKLVQONIFTAMQAMTRAMDTRKIPYKEHNKAHQOLVREVDVEKVSAFENPV 129
Db 73 EERKGRPLVQONIFSMRAMEAMERLQIPSPRSPEKHSLVMSODPYKTYFERRYA 132

Qy 10 C1SEEKEARINDEERHVRDKRDRARREKLILLGTEGESSKSTFKOMRITHGSGSD 69
Db 13 C1TEDEKAARVQDQEINRILLFQKQDRGEKLILLGPGESSKSTFKOMRITHGAGYE 72
Qy 70 EDRKRGFTKLVQONIFTAMQAMTRAMDTRKIPYKEHNKAHQOLVREVDVEKVSAFENPV 129
Db 73 EERKGRPLVQONIFSMRAMEAMERLQIPSPRSPEKHSLVMSODPYKTYFERRYA 132

Qy 130 DAISLWNDPGQIQCYDRREYQVLSDSTKYYLNDLDRVADPAVLPTQDVLVRYRPTGI 189
Db 133 AMQWLWRDAGIRACYERRREFHLLSDAVVYLSHLERITEEGVYVPTAQDVLRSRMPITGI 192

Qy 190 TEPFDLQSIFRMVMDQGQSRERRWIKHCENUTSIMFLVSEYDQVLFDSNEMRE 249
Db 193 NEYCFSVQKTNLIVGQGQSKERKWHCENUTSIMFLVSEYDQVLFDSNEMRE 252

Qy 250 ESKALFRITYPWQFQNSVILLVNLKKDLLEEKIMYSHLVDYPEYDQFORDQAAREFI 309
Db 253 ESLALFGTILDPWFKSTSVILFLNKDILBEPKIPSHLATEYFSPSFGPKDAAKRFI 312

Qy 310 KMFVDL-----NPDSD-----KIIYSHFTCATDENTIREVFAAYKDTIQLNLKEYN 357
Db 313 LDMDTRMTGVDGPEGSNRNRKETKEIYSHFTCATDNNIQFVDAVTDVIONNLKYIG 372

Qy 358 L 358
Db 373 L 373

RESULT 12
US-09-442-349A-22

Sequence 24; Application US/09442349A
Patent No. 6462178
GENERAL INFORMATION:
APPLICANT: Wong, Yung H
TITLE OF INVENTION: G Protein
FILE REFERENCE: M9/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 374

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: G protein
OTHER INFORMATION: chimera

US-09-442-349A-24

Query Match 57.0%; Score 1061; DB 4; Length 374;
Best Local Similarity 57.1%; Pred. No. 2.5e-99;
Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;

GENERAL INFORMATION:
APPLICANT: Wong, Yung H
TITLE OF INVENTION: G Protein
FILE REFERENCE: M9/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 374

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: G protein
OTHER INFORMATION: chimera

Qy 10 C1SEEKEARINDEERHVRDKRDRARREKLILLGTEGESSKSTFKOMRITHGSGSD 69
Db 13 C1TEDEKAARVQDQEINRILLFQKQDRGEKLILLGPGESSKSTFKOMRITHGAGYE 72
Qy 70 EDRKRGFTKLVQONIFTAMQAMTRAMDTRKIPYKEHNKAHQOLVREVDVEKVSAFENPV 129
Db 73 EERKGRPLVQONIFSMRAMEAMERLQIPSPRSPEKHSLVMSODPYKTYFERRYA 132

Qy 130 DAISLWNDPGQIQCYDRREYQVLSDSTKYYLNDLDRVADPAVLPTQDVLVRYRPTGI 189
Db 133 AMQWLWRDAGIRACYERRREFHLLSDAVVYLSHLERITEEGVYVPTAQDVLRSRMPITGI 192

Qy 190 TEPFDLQSIFRMVMDQGQSRERRWIKHCENUTSIMFLVSEYDQVLFDSNEMRE 249

RESULT 13
US-09-442-349A-33

Sequence 33, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442, 349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 26
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: G protein
; OTHER INFORMATION: chimera

US-09-442-349A-33

Query Match 56.9%; Score 1058; DB 4; Length 374;
Best Local Similarity 57.1%; Pred. No. 5e-99;
Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2

Qy 10 CLESEEAKEARRNDEIEHRVRDKDRARRELKILLGKGESCKSTIKOMRTHGSGYSD 69
Db 13 CLEDEKAARYDOEINRILLEQKDRGELKILLGKGESCKSTIKOMRTHGAGYSE 72
Qy 70 EDRKGFRPLVYQVNPYNSMRMTEAMERLOQPSRSPSKHHASLMSDQPYKVTEKRYA 132
Db 73 EDRKGFRPLVYQVNPYNSMRMTEAMERLOQPSRSPSKHHASLMSDQPYKVTEKRYA 132
Qy 130 DAISLWNDPGQECYRREQLSOSTKYYNDLDRVADPAVLQDQDVIRVPTGI 189
Db 133 AAMQWLRDAGTRACYERREHLLSAYVYSHLRITERGCVYQPAQDVRSRMPITGI 192
Qy 190 IEPFDLQSVTRMDVGGQRERRKWHCFENVTSMFLVALSEYDQVLYBESDNRME 249
Db 193 NEYCFSVQTKNIRIVDGGQSKERRKWHCFENVTIYLASLESDQCLEENQENRMRK 252
Qy 191 IEPFDLQSVTRMDVGGQRERRKWHCFENVTSMFLVALSEYDQVLYBESDNRME 249
Db 193 NEYCFSVQTKNIRIVDGGQSKERRKWHCFENVTIYLASLESDQCLEENQENRMRK 252
Qy 192 IEPFDLQSVTRMDVGGQRERRKWHCFENVTSMFLVALSEYDQVLYBESDNRME 249
Db 193 NEYCFSVQTKNIRIVDGGQSKERRKWHCFENVTIYLASLESDQCLEENQENRMRK 252
Qy 250 ESKALFRTITYPWFQNSVFLNKKDLERKIMSHLVDYFPEPDGPOQDAQAREFTI 309
Db 253 ESLALFGTILELPWFKSTISVLFLNKDILEKIPFISHLATYFPSQGPKDAAKRFI 312
Qy 310 LKMFVDL-----NPQSD-----KLYSHFCATDENIREVFAVKTDLQNLKEYN 357
Db 313 LDNYTRMYTGCVDGPEGSNRNRKETKEYSHFCATDENIQFVNAYTDVIIQNLKYIG 372
Qy 358 L 358
Db 373 L 373

RESULT 14
US-09-442-349A-26

Sequence 26, Application US/09442349A
; Sequence 26, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442, 349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 26
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: G protein
; OTHER INFORMATION: chimera

US-09-442-349A-26

Query Match 56.9%; Score 1058; DB 4; Length 374;
Best Local Similarity 57.1%; Pred. No. 5e-99;
Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2

Qy 10 CLESEEAKEARRNDEIEHRVRDKDRARRELKILLGKGESCKSTIKOMRTHGSGYSD 69
Db 13 CLEDEKAARYDOEINRILLEQKDRGELKILLGKGESCKSTIKOMRTHGAGYSE 72
Qy 70 EDRKGFRPLVYQVNPYNSMRMTEAMERLOQPSRSPSKHHASLMSDQPYKVTEKRYA 132
Db 73 EDRKGFRPLVYQVNPYNSMRMTEAMERLOQPSRSPSKHHASLMSDQPYKVTEKRYA 132
Qy 130 DAISLWNDPGQECYRREQLSOSTKYYNDLDRVADPAVLQDQDVIRVPTGI 189
Db 133 AAMQWLRDAGTRACYERREHLLSAYVYSHLRITERGCVYQPAQDVRSRMPITGI 192
Qy 190 IEPFDLQSVTRMDVGGQRERRKWHCFENVTSMFLVALSEYDQVLYBESDNRME 249
Db 193 NEYCFSVQTKNIRIVDGGQSKERRKWHCFENVTIYLASLESDQCLEENQENRMRK 252
Qy 191 IEPFDLQSVTRMDVGGQRERRKWHCFENVTSMFLVALSEYDQVLYBESDNRME 249
Db 193 NEYCFSVQTKNIRIVDGGQSKERRKWHCFENVTIYLASLESDQCLEENQENRMRK 252
Qy 192 IEPFDLQSVTRMDVGGQRERRKWHCFENVTSMFLVALSEYDQVLYBESDNRME 249
Db 193 NEYCFSVQTKNIRIVDGGQSKERRKWHCFENVTIYLASLESDQCLEENQENRMRK 252
Qy 250 ESKALFRTITYPWFQNSVFLNKKDLERKIMSHLVDYFPEPDGPOQDAQAREFTI 309
Db 253 ESLALFGTILELPWFKSTISVLFLNKDILEKIPFISHLATYFPSQGPKDAAKRFI 312
Qy 310 LKMFVDL-----NPQSD-----KLYSHFCATDENIREVFAVKTDLQNLKEYN 357
Db 313 LDNYTRMYTGCVDGPEGSNRNRKETKEYSHFCATDENIQFVNAYTDVIIQNLKYIG 372
Qy 358 L 358
Db 373 L 373

RESULT 15
US-09-442-349A-28

Sequence 28, Application US/09442349A
; Sequence 28, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442, 349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 28
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequence: G protein
; OTHER INFORMATION: chimera

US-09-442-349A-28

Best Local Similarity 57.1%; Pred. No. 5e-99; Matches 206; Conservative 56; Mismatches 87; Indels 12; Gaps 2;

Qy 10 CLSEAKERARRNDBIERVYRDKRDRARBLKLULGEGSKSTFIKOMRIIHGSYSSD 69
 Db 13 CLTBDEKAARVDOBEINRLLQEQKDRBKLULGEGSKSTFIKOMRIINGAGSS 72

Qy 70 EDKRGFTKLYQNIIFTAMQMRAMDTLKYKTEHNKAHQLYREVDEKVSAGENPV 129
 Db 73 EERGFPRPLYQNTFVSMRAMEMLRQIPFSRPESKHHSALVMSQDLYKVTIFKRYA 132

Qy 130 DAIKSLWNPGIQRCYDRREYQLDSTKYLYNLDRVADPAYLPTQDYLRVKPTG 189
 Db 133 AAMONLWRDAGIRACIERRFHLDLSAYYLSHLERITFEGYVPTAQDYLRSRPTG 192

Qy 190 IEYPRDLSQVIFRMVDGCGSRERKWKICFENYTSIMTVLASEYDOLVSESNERAE 249

Qy 193 NEYCFSVQKTNLRITDVGQSKERKWKICFENYVIALTIASTUSBYDQLEENQENR 252

Db 250 ESKALFRITITYPWFQNSVILFLNKDLKLEKIMYSWJYDYPEDGQDQAAREI 309
 Db 253 ESLALFGTILELPWFKSTSVLFLNKTDLEEKIPTSHLATYFSPSFQGPKQDAAKRFI 312

Qy 310 LKMFVDL-----NPDS-----KIIYHFTCATDTENTRFVIAAVKOTIQLNKEVN 357

Db 313 LDWVTRMYTQCVDGEGPSRNKETKEIYSHFTCATDTICNQFVQAVTUVIONNLKYIG 372

Qy 358 L 358

Db 373 L 373

Search completed: June 30, 2003, 16:18:45
 Job time : 16 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: June 30, 2003, 16:16:21 ; Search time 24 Seconds
 (without alignments)
 1640.134 Million cell updates/sec

Title: US-09-899-295-2
 Perfect score: 1860
 Sequence: 1 MTLESIMACCLSEERKEARR... VFAAVKDTILQLNLKEYNLV 359

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_AA:*

1: /cn2_6/ptodata/2/pubpaa/us08_NEWPUB.pep:*

2: /cn2_6/ptodata/2/pubpaa/PCT_NEWPUB.pep:*

3: /cn2_6/ptodata/2/pubpaa/US06_NEWPUB.pep:*

4: /cn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cn2_6/ptodata/2/pubpaa/US07_NEWPUB.pep:*

6: /cn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

8: /cn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cn2_6/ptodata/2/pubpaa/US09_NEWPUB.pep:*

10: /cn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cn2_6/ptodata/2/pubpaa/US10_NEWPUB.pep:*

12: /cn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

13: /cn2_6/ptodata/2/pubpaa/us360_NEWPUB.pep:*

14: /cn2_6/ptodata/2/pubpaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
 US-09-899-295-2
 ; Sequence 2, Application US-098999295
 ; Patent No. US20030127601A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aventis Pharma Deutschland GmbH
 ; TITLE OF INVENTION: Process for identifying modulators of G protein coupled receptors
 ; FILE REFERENCE: AVE D-2000/A033 englisch
 ; CURRENT APPLICATION NUMBER: US09/899,295
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Mus musculus

US-09-899-295-2

ALIGNMENTS

SUMMARIES

Result	Score	Query Match	Length	DB ID	Description
1	1860	100.0	359	10	US-09-899-295-2
2	1846	99.2	359	10	US-09-984-292-1
3	1846	99.2	359	10	US-09-989-497-1
4	1842	99.0	359	10	US-09-984-292-37
5	1842	99.0	359	10	US-09-984-497-37
6	1837	98.8	359	10	US-09-984-292-15
7	1837	98.8	359	10	US-09-984-497-15
8	1822	98.0	359	10	US-09-984-292-9
9	1822	98.0	359	10	US-09-984-497-9
10	1819	97.8	353	10	US-09-984-292-2
11	1819	97.8	353	10	US-09-984-497-2
12	1818	97.7	359	10	US-09-984-292-21
13	1818	97.7	359	10	US-09-989-497-21
14	1817	97.7	353	9	US-09-952-680A-27
15	1817	97.7	353	10	US-09-94-292-16
16	1817	97.7	353	10	US-09-984-497-16
17	1815	97.6	359	10	US-09-984-497-11
18	1815	97.6	359	10	US-09-984-497-11
19	1814	97.5	353	10	US-09-899-295-8
20	1814	97.5	353	10	US-09-894-292-26
21	1813	97.5	359	10	US-09-984-497-26
22	1813	97.5	359	10	US-09-984-292-3
23	1811	97.4	359	10	US-09-989-497-3
24	1811	97.4	359	10	US-09-989-497-4
25	1810	97.3	353	10	US-09-898-497-10
26	1807	97.2	359	10	US-09-984-292-4
27	1807	97.2	359	10	US-09-989-497-20
28	1806	97.1	359	10	US-09-984-292-25
29	1806	97.1	359	10	US-09-989-497-25
30	1804	97.0	359	10	US-09-984-292-10
31	1803	96.9	359	10	US-09-984-292-22
32	1803	96.9	359	10	US-09-984-292-22
33	1803	96.9	359	10	US-09-984-292-22
34	1800	96.8	359	10	US-09-989-497-12
35	1800	96.8	359	10	US-09-989-497-12
36	1795	96.5	353	10	US-09-984-292-8
37	1795	96.5	353	10	US-09-984-497-8
38	1793	96.4	359	10	US-09-984-292-13
39	1793	96.4	359	10	US-09-989-497-13
40	1791	96.3	353	10	US-09-984-292-17
41	1791	96.3	353	10	US-09-989-497-17
42	1789	96.2	359	10	US-09-984-292-23
43	1789	96.2	359	10	US-09-989-497-23
44	1784	95.9	353	10	US-09-984-292-4
45	1784	95.9	353	10	US-09-984-292-5

RESULT 2
US-09-984-292-1
Sequence 1, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984, 292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243, 770
; PRIORITY FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-984-292-1

Query Match 99.2%; Score 1846; DB 10; Length 359;
Best Local Similarity 99.2%; Pred. No. 2.7e-148; 2; Mismatches 1; Indels 0; Gaps 0;
Matches 356; Conservative 1; Mis 0; Gap 0;
; Query 1 MTLESIMACCLSEEAKEARRINDETERHYRDRKDRARRELKLULLGGESEGSKSTFIQMR 60
; Db 1 MTLESIMACCLSEEAKEARRINDETERQRLRDRKDRARRELKLULLGGESEGSKSTFIQMR 60
; Query 61 IINGSGYSDEDKRGTFLKYQNIFTAMQAMIRANDTLPKYEHNKHAQLYREVDYK 120
; Db 61 IINGSGYSDEDKRGTFLKYQNIFTAMQAMIRANDTLPKYEHNKHAQLYREVOKE 120
; Query 121 VSAPENPYDAIKSLWNPDQGIQECYDQRKEYQSLSDSTKYLNDLDRWADPSYLPDQV 180
; Db 121 VSAPENPYDAIKSLWNPDQGIQECYDQRKEYQSLSDSTKYLNDLDRWADPSYLPDQV 180
; Query 181 RVRVPTGTIEYPFDLQSVIFRMVDGGQRSERRKWTHCFENTYSIMFLVASEYDQVL 240
; Db 181 RVRVPTGTIEYPFDLQSVIFRMVDGGQRSERRKWTHCFENTYSIMFLVASEYDQVL 240
; Query 241 ESDNENRMEESKALFRTITYPWFQNSVILFLNKDLEEKIMYSHLVDPEYDQVR 300
; Db 241 ESDNENRMEESKALFRTITYPWFQNSVILFLNKDLEEKIMYSHLVDPEYDQVR 300
; Query 301 DAQAREFTLKMFDLNPDSKDTIYSHFTCATOTENIREVFAAVKDTIQLNKEYLV 359
; Db 301 DAQAREFTLKMFDLNPDSKDTIYSHFTCATOTENIREVFAAVKDTIQLNKEYLV 359
; RESULT 3
US-09-889-497-1
Sequence 1, Application US/09989497
; Patent No. US2002013151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/989, 497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/243, 770
; PRIORITY FILING DATE: 2001-10-29

Query Match 99.0%; Score 1842; DB 10; Length 359;
Best Local Similarity 99.2%; Pred. No. 5.9e-18; 1; Mismatches 2; Indels 0; Gaps 0;
Matches 356; Conservative 1; Mis 2; Gap 0;
; Query 1 MTLESIMACCLSEEAKEARRINDETERHYRDRKDRARRELKLULLGGESEGSKSTFIQMR 60
; Db 1 MTLESIMACCLSEEAKEARRINDETERQRLRDRKDRARRELKLULLGGESEGSKSTFIQMR 60
; Query 61 IINGSGYSDEDKRGTFLKYQNIFTAMQAMIRANDTLPKYEHNKHAQLYREVDYK 120
; Db 61 IINGSGYSDEDKRGTFLKYQNIFTAMQAMIRANDTLPKYEHNKHAQLYREVDYK 120

QY 121 VSAFENPYDAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 121 VSAFENPYDAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 QY 181 RVRVPTGIEYPDQLQSIVFMRMVGGRSERRKWIFHENVTSMFLVALSEYDQVL 240
 181 RVRVPTGIEYPDQLQSIVFMRMVGGRSERRKWIFHENVTSMFLVALSEYDQVL 240
 Db 181 VSAFENPYDAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 QY 241 ESDNENRMEESKAFLERTITYPWFQNSVILFLNKDLLEEKIMSHLVDIFFBYDGQR 300
 241 ESDNENRMEESKAFLERTITYPWFQNSVILFLNKDLLEEKIMSHLVDIFFBYDGQR 300
 Db 301 DAQAREFILKMFVDLNPSDKINSHFTCATDTENIRVFAAVKDTIQLNLKEYNV 359
 301 DAQAREFILKMFVDLNPSDKINSHFTCATDTENIRVFAAVKDTIQLNLKEYNV 359

RESULT 5

US-09-980-497-37

; Sequence 37, Application US/09989497

; Patent No. US2002012843A1

; GENERAL INFORMATION:

; APPLICANT: YAO, YONG

; APPLICANT: XU, HONG

; APPLICANT: XU, HONG

; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE

; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF

; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS

; FILE REFERENCE: 078003 028649

; CURRENT APPLICATION NUMBER: US/09/984,292

; CURRENT FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 60/243,770

; PRIOR FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 15

; LENGTH: 359

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-980-497-37

; Query Match

; Best Local Similarity

; Score 98.8%;

; DB 10;

; Length 359;

; Matches 355; Conservative

; Pred. No. 1; 6e-147;

; Mismatches 3;

; Indels 0;

; Gaps 0;

; Query 1

; MTLESIMACCLSEEKAEARRINDETERHVRDRKDRARRELKLILLGTEGSKSTFIKMR 60

; Db 1 MTLESIMACCLSEEKAEARRINDETERHVRDRKDRARRELKLILLGTEGSKSTFIKMR 60

; Query 61

; IHGSGYSDEDKRGFTKLYQNTFAMQAMIRAMDTLKIPYEHNKAHQLYREVDEK 120

; Db 61 IHGSGYSDEDKRGFTKLYQNTFAMQAMIRAMDTLKIPYEHNKAHQLYREVDEK 120

; Query 121

; VSAFENPYDAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVL 180

; Db 121 VSAFENPYDAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVL 180

; Query 181

; RVRVPTGIEYPDQLQSIVFMRMVGGRSERRKWIFHENVTSMFLVALSEYDQVL 240

; Db 181 RVRVPTGIEYPDQLQSIVFMRMVGGRSERRKWIFHENVTSMFLVALSEYDQVL 240

; Query 241

; ESDNENRMEESKAFLERTITYPWFQNSVILFLNKDLLEEKIMSHLVDIFFBYDGQR 300

; Db 241 ESDNENRMEESKAFLERTITYPWFQNSVILFLNKDLLEEKIMSHLVDIFFBYDGQR 300

; Query 301

; DAQAREFILKMFVDLNPSDKINSHFTCATDTENIRVFAAVKDTIQLNLKEYNV 359

; Db 301 DAQAREFILKMFVDLNPSDKINSHFTCATDTENIRVFAAVKDTIQLNLKEYNV 359

; Query 301

; DAQAREFILKMFVDLNPSDKINSHFTCATDTENIRVFAAVKDTIQLNLKEYNV 359

US-09-994-292-15
 ; Sequence 15, Application US/09984292
 ; Patent No. US2003012843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
 ; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
 ; FILE REFERENCE: 078003 028649
 ; CURRENT APPLICATION NUMBER: US/09/984,292
 ; CURRENT FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 60/243,770
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 15
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-984-292-15
 ; Query Match

98.8%	Score 1837;	DB 10;	Length 359;
98.9%	Pred. No. 1; 6e-147;	Mismatches 3;	Indels 0;
98.9%	Best Local Similarity	1;	Gaps 0;
98.9%	Matches 355;	Conservative	

; Matches 355; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTLESIMACCLSEEKAEARRINDETERHVRDRKDRARRELKLILLGTEGSKSTFIKMR 60
 Db 1 MTLESIMACCLSEEKAEARRINDETERHVRDRKDRARRELKLILLGTEGSKSTFIKMR 60

QY 61 IHGSGYSDEDKRGFTKLYQNTFAMQAMIRAMDTLKIPYEHNKAHQLYREVDEK 120
 Db 61 IHGSGYSDEDKRGFTKLYQNTFAMQAMIRAMDTLKIPYEHNKAHQLYREVDEK 120

QY 121 VSAFENPYDAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVL 180
 Db 121 VSAFENPYDAIKSLWNPDGQIQCYDRREYQQLSDSTKYLNDLDRVADPAVLPTQDVL 180

QY 181 RVRVPTGIEYPDQLQSIVFMRMVGGRSERRKWIFHENVTSMFLVALSEYDQVL 240
 Db 181 RVRVPTGIEYPDQLQSIVFMRMVGGRSERRKWIFHENVTSMFLVALSEYDQVL 240

QY 241 ESDNENRMEESKAFLERTITYPWFQNSVILFLNKDLLEEKIMSHLVDIFFBYDGQR 300
 Db 241 ESDNENRMEESKAFLERTITYPWFQNSVILFLNKDLLEEKIMSHLVDIFFBYDGQR 300

QY 301 DAQAREFILKMFVDLNPSDKINSHFTCATDTENIRVFAAVKDTIQLNLKEYNV 359
 Db 301 DAQAREFILKMFVDLNPSDKINSHFTCATDTENIRVFAAVKDTIQLNLKEYNV 359

RESULT 7

US-09-980-497-15

; Sequence 15, Application US/09989497

; Patent No. US2003014315A1

; GENERAL INFORMATION:

; APPLICANT: YAO, YONG

; APPLICANT: XU, HONG

; APPLICANT: XU, HONG

; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE

; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF

; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS

; FILE REFERENCE: 078003 028649

; CURRENT APPLICATION NUMBER: US/09/989,497

; CURRENT FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 09/984,292

; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 60/243,770

; PRIOR FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 15

; LENGTH: 359

; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-989-497-15

Query Match 98.8%; Score 1837; DB 10; Length 359;
Best Local Similarity 98.9%; Pred. No. 1.6e-147;
Matches 355; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MTLESIMACCLSEEAKEARRINDEIERVRDKRDARRELKULLLGTEGSGKSTFIQMR 60
Db 1 MTLESIMACCLSEEAKEARRINDEIERVRDKRDARRELKULLLGTEGSGKSTFIQMR 60

Qy 61 ITHGSGYSDEDKRGFTKLVYQNFITAMQAMIRAMDTLKIPYKEHNKAHAQLREVDEK 120
Db 61 ITHGSGYSDEDKRGFTKLVYQNFITAMQAMIRAMDTLKIPYKEHNKAHAQLREVDEK 120

Db 61 ITHGSGYSDEDKRGFTKLVYQNFITAMQAMIRAMDTLKIPYKEHNKAHAQLREVDEK 120

Qy 121 VSAFENPYDVAIKSLWNPQIQCYDRREYQLSDTKYLDRADPSYLTQDVL 180
Db 121 VSAFENPYDVAIKSLWNPQIQCYDRREYQLSDTKYLDRADPSYLTQDVL 180

Qy 121 VSAFENPYDVAIKSLWNPQIQCYDRREYQLSDTKYLDRADPSYLTQDVL 180

Qy 181 RVRVPTTGIEIYPFDLQSVIFRMVGQSRERKWKHCFENVTSMFLVALSEYDQVL 240
Db 181 RVRVPTTGIEIYPFDLQSVIFRMVGQSRERKWKHCFENVTSMFLVALSEYDQVL 240

Db 181 RVRVPTTGIEIYPFDLQSVIFRMVGQSRERKWKHCFENVTSMFLVALSEYDQVL 240

Qy 241 ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLEEKIMYSHLVDYFPEYDQMR 300
Db 241 ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLEEKIMYSHLVDYFPEYDQMR 300

Qy 301 DAOAREFILKMFVDLNPDSKIIYSHFTCATDTENRFVAVKDTILQLNLKEYNLV 359
Db 301 DAOAREFILKMFVDLNPDSKIIYSHFTCATDTENRFVAVKDTILQLNLKEYNLV 359

RESULT 9
US-09-989-497-9

Sequence 9, Application US/09989497
; Patent No. US20020143151A1

GENERAL INFORMATION:

APPLICANT: YAO, YONG

APPLICANT: XU, HONG

APPLICANT: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE

TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF

TITLE OF INVENTION: CHEMOSENSORY RECEPTORS

FILE REFERENCE: 078003-0280735

CURRENT APPLICATION NUMBER: US/09/989, 497

PRIOR APPLICATION NUMBER: 09/984, 292

PRIOR FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 60/243, 770

PRIOR FILING DATE: 2000-10-30

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 9

LENGTH: 359

TYPE: PRT

ORGANISM: MUS SP.

US-09-989-497-9

Query Match 98.0%; Score 1822; DB 10; Length 359;

Best Local Similarity 98.3%; Pred. No. 2.9e-146;

Matches 353; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MTLESIMACCLSEEAKEARRINDEIERVRDKRDARRELKULLLGTEGSGKSTFIQMR 60
Db 1 MTLESIMACCLSEEAKEARRINDEIERVRDKRDARRELKULLLGTEGSGKSTFIQMR 60

Db 61 ITHGSGYSDEDKRGFTKLVYQNFITAMQAMIRAMDTLKIPYKEHNKAHAQLREVDEK 120
Qy 61 ITHGSGYSDEDKRGFTKLVYQNFITAMQAMIRAMDTLKIPYKEHNKAHAQLREVDEK 120

Db 121 VSAFENPYDVAIKSLWNPQIQCYDRREYQLSDTKYLDRADPSYLTQDVL 180
Qy 121 VSAFENPYDVAIKSLWNPQIQCYDRREYQLSDTKYLDRADPSYLTQDVL 180

Db 121 VSAFENPYDVAIKSLWNPQIQCYDRREYQLSDTKYLDRADPSYLTQDVL 180

Qy 181 RVRVPTTGIEIYPFDLQSVIFRMVGQSRERKWKHCFENVTSMFLVALSEYDQVL 240
Db 181 RVRVPTTGIEIYPFDLQSVIFRMVGQSRERKWKHCFENVTSMFLVALSEYDQVL 240

Db 181 RVRVPTTGIEIYPFDLQSVIFRMVGQSRERKWKHCFENVTSMFLVALSEYDQVL 240

Qy 241 ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLEEKIMYSHLVDYFPEYDQMR 300
Db 241 ESDNENRMEESKALFRTTITYPWFQNSVILFLNKDLEEKIMYSHLVDYFPEYDQMR 300

Qy 301 DAOAREFILKMFVDLNPDSKIIYSHFTCATDTENRFVAVKDTILQLNLKEYNLV 359
Db 301 DAOAREFILKMFVDLNPDSKIIYSHFTCATDTENRFVAVKDTILQLNLKEYNLV 359

RESULT 10
US-09-984-292-2

Sequence 2, Application US/09984292

; Patent No. US20020128433A1

GENERAL INFORMATION:

APPLICANT: YAO, YONG

APPLICANT: XU, HONG

TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE

RESULT 11
 US-09-989-497-2
 ; Sequence 2, Application US/09989497
 ; Patent No. US2002143151A1

GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
 ; ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; CHEMOSENSORY RECEPTORS

FILE REFERENCE: 078003-0280649
 CURRENT FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: 09/984, 292
 PRIOR FILING DATE: 2001-10-29
 PRIOR APPLICATION NUMBER: 60/243, 770
 PRIOR FILING DATE: 2000-10-30
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 353
 TYPE: PRT
 ; ORGANISM: Mus sp.
 ; US-09-984-292-2

Query Match 97.8%; Score 1819; DB 10; Length 353;
 Best Local Similarity 99.2%; Pred. No. 5.1e-146; 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 350; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Query Match 97.8%; Score 1819; DB 10; Length 353;
 Best Local Similarity 99.2%; Pred. No. 5.1e-146; 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 350; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 MACCISEEAKEARRINDEERHVRDKDRARREKLILLGTGESGKSTIKQMRTHSG 66
 1 MACCISEEAKEARRINDEERHVRDKDRARREKLILLGTGESGKSTIKQMRTHSG 60

QY 67 YSDEDKRGFTKLVYONIFTAMQAMTRAMDTLKIPIKYEHINKAHQVLREVDEKVSFEN 126
 61 YSDEDKRGFTKLVYONIFTAMQAMTRAMDTLKIPIKYEHINKAHQVLREVDEKVSFEN 120

QY 127 PYVDAIKSLNNDPGIQCYCRREYOLSPSTKYYLNDLDRVADPAVLPPQDVLVRPT 185
 1 MACCISEEAKEARRINDEERHVRDKDRARREKLILLGTGESGKSTIKQMRTHSG 60

QY 67 YSDEDKRGFTKLVYONIFTAMQAMTRAMDTLKIPIKYEHINKAHQVLREVDEKVSFEN 126
 61 YSDEDKRGFTKLVYONIFTAMQAMTRAMDTLKIPIKYEHINKAHQVLREVDEKVSFEN 120

Db 127 PYVDAIKSLNNDPGIQCYCRREYOLSPSTKYYLNDLDRVADPAVLPPQDVLVRPT 185
 1 MACCISEEAKEARRINDEERHVRDKDRARREKLILLGTGESGKSTIKQMRTHSG 60

QY 187 TGIEYPFDLQSVIRFMVYGGQSERRKWICHCEVNSTMFLVALSETDQVLVESDEN 246
 121 PYVDAIKSLNNDPGIQCYCRREYOLSPSTKYYLNDLDRVADPAVLPPQDVLVRPT 180

QY 187 TGIEYPFDLQSVIRFMVYGGQSERRKWICHCEVNSTMFLVALSETDQVLVESDEN 246
 181 TGIEYPFDLQSVIRFMVYGGQSERRKWICHCEVNSTMFLVALSETDQVLVESDEN 240

Db 247 RMEESKALFRITITYPWFQNSVILFLNKDLLEKIMSHLVYFPEVDGPQDAAR 306
 241 RMEESKALFRITITYPWFQNSVILFLNKDLLEKIMSHLVYFPEVDGPQDAAR 306

QY 307 EFTLKMFDVLNPDSKIIYSHFTCATDTENIRFVAAVDTIQLNLKEYNLV 359
 301 EFTLKMFDVLNPDSKIIYSHFTCATDTENIRFVAAVDTIQLNLKEYNLV 353

RESULT 12
 US-09-984-292-21
 ; Sequence 21, Application US/09984292
 ; Patent No. US2002143151A1

GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
 ; ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; CHEMOSENSORY RECEPTORS

FILE REFERENCE: 078003-0280649
 CURRENT FILING DATE: 2001-10-29
 PRIOR APPLICATION NUMBER: 60/243, 770
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 21
 LENGTH: 359
 TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-984-292-21

Query Match 97.7%; Score 1818; DB 10; Length 359;
 Best Local Similarity 98.3%; Pred. No. 5.3e-146; 5; Mismatches 1; Indels 0; Gaps 0;
 Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLESIMACCISEEAKEARRINDEERHVRDKDRARREKLILLGTGESGKSTIKQMR 60
 1 MTLESIMACCISEEAKEARRINDEERHVRDKDRARREKLILLGTGESGKSTIKQMR 60

Db 61 ITHGSSYSDEDKRGFTKLVYONIFTAMQAMTRAMDTLKIPIKYEHINKAHQVLREVDEKVSFEN 120
 61 ITHGSSYSDEDKRGFTKLVYONIFTAMQAMTRAMDTLKIPIKYEHINKAHQVLREVDEKVSFEN 120

QY 181 RVRVPITGIEYPFDLQSVIRFMVYGGQSERRKWICHCEVNSTMFLVALSETDQVLV 240
 181 RVRVPITGIEYPFDLQSVIRFMVYGGQSERRKWICHCEVNSTMFLVALSETDQVLV 240

Db 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDLLEKIMSHLVYFPEVDGPQ 300
 241 ESDNENRMEESKALFRITITYPWFQNSVILFLNKDLLEKIMSHLVYFPEVDGPQ 300

QY 301 DAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVAAVDTIQLNLKEYNLV 359

Db 301 DAQAREFILKMFVLNPDSDKIYSHFTCATDENTIREVFAVKTDLQLNKEYNLV ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 27 ; LENGTH: 353 ;
; Sequence 21, Application US/09989497 ;
; General Information: ;
; Patent No. US20020143151A1 ;
; Applicant: YAO, YONG ;
; Title of Invention: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS ;
; Title of Invention: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS ;
; File Reference: 078003 0280735 ;
; Current Application Number: US/09/989,497 ;
; Prior Application Number: 09/984,292 ;
; Prior Filing Date: 2001-10-29 ;
; Prior Application Number: 60/243,770 ;
; Prior Filing Date: 2000-10-30 ;
; Software: Patentin Ver. 2.1 ;
; Seq ID No 21 ;
; Length: 359 ;
; Organism: Homo sapiens ;
; US-09-989-97-21 ;
; Query Match 97.7%; Score 1818; DB 10; Length 359;
; Best Local Similarity 98.3%; Pred. No. 6.3e-146; Indels 0; Gaps 0;
; Matches 353; Conservative 1; Mismatches 5;
; Qy 1 MTLESIMACCLSEEKEARRINDETERHYRDKDRARRELKLILLGTGESGKSPFIKOMR 60
; Db 1 MTLESIMACCLSEEKEARRINDETERHYRDKDRARRELKLILLGTGESGKSPFIKOMR 60
; Qy 61 IIGSSGYSDBEDKRGFTKLVYQNTAMQAMIRAMDTLKYPIKYEHNKHAQLYREDEVK 120
; Db 61 IIGSSDYSEEDKRGFTKLVYQNTAMQAMIRAMDTLKYPIKYEHNKHAQLYREDEVK 120
; Qy 121 VSAFENPYDAIKSLWNPDGQIQCYDRREYQSDSTKYLNDLDRVADPAYLPTQDVL 180
; Db 121 VSAFENPYDAIKSLWNPDGQIQCYDRREYQSDSTKYLNDLDRVADPAYLPTQDVL 180
; Qy 121 VSARFDVDPYDAIKSLWNPDGQIQCYDRREYQSDSTKYLNDLDRVADPAYLPTQDVL 180
; Db 121 VSARFDVDPYDAIKSLWNPDGQIQCYDRREYQSDSTKYLNDLDRVADPAYLPTQDVL 180
; Qy 181 RVRPTGTEIYEPDLOSYTFRMDVGSORSERKWKHGFENTYSIMPLVASEYDVLV 240
; Db 181 RVRPTGTEIYEPDLOSYTFRMDVGSORSERKWKHGFENTYSIMPLVASEYDVLV 240
; Qy 241 ESDENRMEESKAFLERTITYPWFONSSVILFLNKDLBEEKIMSHLVDFPEYDGPOR 300
; Db 241 ESDENRMEESKAFLERTITYPWFONSSVILFLNKDLBEEKIMSHLVDFPEYDGPOR 300
; Qy 301 DAQAREFILKMFVLNPDSDKIYSHFTCATDENTIREVFAVKTDLQLNKEYNLV 359
; Db 301 DAQAREFILKMFVLNPDSDKIYSHFTCATDENTIREVFAVKTDLQLNKEYNLV 359
; Result 14 ;
; US-09-952-680A-27 ;
; Sequence 27, Application US/09952680A ;
; General Information: ;
; Publication No. US20030087239A1 ;
; Applicant: Stanton, Marty ;
; Applicant: Epstein, David ;
; Applicant: Hamaguchi, No. US20030087239A1 ;
; Title of Invention: Target Activated Biosensor and Methods of Using Same ;
; File Reference: 23239-501 ;
; Current Application Number: US/09/952,680A ;
; Current Filing Date: 2001-09-13 ;
; Prior Application Number: 60/232,454 ;
; Prior Filing Date: 2000-09-13 ;
; Number of Seq ID Nos: 75 ;
; US-09-984-292-16 ;
; Query Match 97.7%; Score 1817; DB 10; Length 353;
; Best Local Similarity 99.2%; Pred. No. 7.5e-146; Indels 0; Gaps 0;
; Matches 350; Conservative 1; Mismatches 2;
; Qy 7 MACCLSEEKEARRINDETERHYRDKDRARRELKLILLGTGESGKSPFIKOMRITGSG 66
; Db 1 MACCLSEEKEARRINDETERHYRDKDRARRELKLILLGTGESGKSPFIKOMRITGSG 66
; Qy 67 YSDEDKRGFTKLVYQNTAMQAMIRAMDTLKYPIKYEHNKHAQLYREDEVKSAFEN 126
; Db 61 YSDEDKRGFTKLVYQNTAMQAMIRAMDTLKYPIKYEHNKHAQLYREDEVKSAFEN 126
; Qy 127 PYVDAIKSLWNPDGQIQCYDRREYQSDSTKYLNDLDRVADPAYLPTQDVLVRVPT 186
; 121 PYVDAIKSLWNPDGQIQCYDRREYQSDSTKYLNDLDRVADPAYLPTQDVLVRVPT 180
; Qy 187 TGIEPYEPDLOSYTFRMVUGGOSEERRWHEFENVISIMFLVALSYDVLVSEN 246
; Db 181 TGIEPYEPDLOSYTFRMVUGGOSEERRWHEFENVISIMFLVALSYDVLVSEN 240
; Qy 247 RMEESKAFLERTITYPWFONSSVILFLNKDLBEEKIMSHLVDFPEYDGPOR 306
; Db 307 EFLIKMFVLNPDSDKIYSHFTCATDENTIREVFAVKTDLQLNKEYNLV 359
; Db 301 EFLIKMFVLNPDSDKIYSHFTCATDENTIREVFAVKTDLQLNKEYNLV 353
; Result 15 ;
; US-09-984-292-16 ;
; Sequence 15, Application US/09984292 ;
; Patent No. US20020128433A1 ;
; General Information: ;
; Applicant: YAO, YONG ;
; Title of Invention: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS ;
; Title of Invention: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS ;
; File Reference: 078003 0280649 ;
; Current Application Number: US/09/984,292 ;
; Current Filing Date: 2001-10-29 ;
; Prior Application Number: 60/243,770 ;
; Prior Filing Date: 2000-10-30 ;
; Software: Patentin Ver. 2.1 ;
; Seq ID No 16 ;
; Length: 353 ;
; Organism: Homo sapiens ;
; US-09-984-292-16 ;
; Query Match 97.7%; Score 1817; DB 10; Length 353;
; Best Local Similarity 99.2%; Pred. No. 7.5e-146; Indels 0; Gaps 0;
; Matches 350; Conservative 1; Mismatches 2;
; Qy 7 MACCLSEEKEARRINDETERHYRDKDRARRELKLILLGTGESGKSPFIKOMRITGSG 66
; Db 1 MACCLSEEKEARRINDETERHYRDKDRARRELKLILLGTGESGKSPFIKOMRITGSG 66
; Qy 67 YSDEDKRGFTKLVYQNTAMQAMIRAMDTLKYPIKYEHNKHAQLYREDEVKSAFEN 126
; Db 61 YSDEDKRGFTKLVYQNTAMQAMIRAMDTLKYPIKYEHNKHAQLYREDEVKSAFEN 126
; Qy 127 PYVDAIKSLWNPDGQIQCYDRREYQSDSTKYLNDLDRVADPAYLPTQDVLVRVPT 186

DB 121 PYVDAIKSLWNDGIQECYDRREYQLSSTDKYLNNDDRVADPAYLTQDVLRVKPT 180
QY 187 TGITEYRFDLQSYIFRMVDVGSRSERKWRKHFENVMSIMFLVALSEYDQVIVESDEN 246
DB 181 TGIEYRFDLQSYIFRMVDVGGRSERKWRKHFENVMSIMFLVALSEYDQVIVESDEN 240
QY 247 RMEESKALFRITTYPWNQNSVILEEKINSHLVYFPEYDGORDAAR 306
DB 241 RMEESKALFRITTYPWNQNSVILEEKINSHLVYFPEYDGORDAAR 300
QY 307 EFLKMFDLNPSDKIYSHFTCATDTEINRVAFKDTIQLNLUKEYNLV 359
DB 301 EFLKMFDLNPSDKIYSHFTCATDTEINRVAFKDTIQLNLUKEYNLV 353

Search completed: June 30, 2003, 16:19:16
Job time : 25 secs



GenCore version 5.1.6
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MM protein - protein search, using sw model

run on: June 30, 2003, 16:14:36 ; Search time 19 Seconds
 (without alignments)
 1816.435 Million cell updates/sec

title: US-09-899-295-2

sequence: 1 MILESIMACCLSEAKEARR. VPAVAKDTILQNLNEKINLV 359

scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

searched: 283224 seqs, 9613422 residues

total number of hits satisfying chosen parameters: 283224

maximum DB seq length: 0
 maximum DB seq length: 200000000

post processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

PIR:73:*

1: Pirl:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

result No.	Score	Query	Match	Length	DB	ID	Description
1	1857	99.8	359	1	RGMSQ		GTP-binding regulatory protein Gq alpha chain - mouse
2	1844	99.1	359	2	S71963		C;Species: Mus musculus (house mouse)
3	1799	96.7	359	2	S45699		C;Accession: A38414
4	1709	91.9	359	2	S30359		PI-Strathmann, M.; Simon, M.I.
5	1685	90.6	359	2	S45700		Proc. Natl. Acad. Sci. U.S.A. 87, 9113-9117, 1990
6	1682	90.4	359	1	RENS11		A;Title: G protein diversity: a distinct class of alpha subunits is present in vertebrates; it is specific for each type of G protein.
7	1681	90.4	359	1	RGHU1		A;Reference number: A38414; MUID:91067657; PMID:2123549
8	1667	89.6	353	2	B0891		A;Accession: A38414
9	1538	82.7	355	2	A40891		A;Molecule type: mRNA
10	1535	82.5	355	2	A41534		A;Residues: 1-359 <STR>
11	1524	81.9	353	2	S34347		A;Cross-references: GB:M55412; NID:gi93501; PID:AAA63306.1; PID:gi93502
12	1513	81.3	355	2	R15288		C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that are found in the beta and gamma chains, required for GTPase activity, appear to be common to all G proteins.
13	1469.5	79.9	354	2	S3309		C;Superfamily: GTP-binding regulatory protein Gs alpha chain
14	1425.5	76.6	360	2	JN0115		C;Keywords: GTP binding; heterotrimeric; nucleotide binding; P-loop; signal transducti
15	1066	57.3	374	2	B41534		F:274-277/Region: GTP-binding NKXD motif
16	1044	56.1	374	2	A41096		F:183/Binding site: GTP (Lys) #status predicted
17	913	49.1	353	2	S71965		F:183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted
18	904	48.6	198	2	S71964		Qy 1 MILESIMACCLSEAKEARRINDETERHYRDKDARRELKLILGTEGSKSTFIKMR 60
19	898.5	48.3	354	1	RGHU1		Db 1 MILESIMACCLSEAKEARRINDETERHYRDKDARRELKLILGTEGSKSTFIKMR 60
20	898.5	48.3	354	1	REBO11		Qy 61 IHGSGYSDEDKRGFTKLYVONIFTAMQAMIRAMDTLKIPIKYKEHNKAHQALYREVDEK 120
21	897.5	48.3	354	1	RGRT1		Db 61 IHGSGYSDEDKRGFTKLYVONIFTAMQAMIRAMDTLKIPIKYKEHNKAHQALYREVDEK 120
22	895.5	48.1	354	2	S40508		Qy 121 VSARENPYVDAIKSLWNPDGQIYCQYDRREYQYQSDSTKYLQNLDRVADPAVYQDVL 180
23	893	48.0	353	2	JC7661		Db 121 VSARENPYVDAIKSLWNPDGQIYCQYDRREYQYQSDSTKYLQNLDRVADPAVYQDVL 180
24	890	47.8	353	1	T50482		Qy 181 RVRYPTGIGIEYPFDQLOSVIYRMDVGGORSERRKWIKHCFENVNTSIMLEVSYDQVL 240
25	888.5	47.8	354	1	REX11		Db 181 RVRYPTGIGIEYPFDQLOSVIYRMDVGGORSERRKWIKHCFENVNTSIMLEVSYDQVL 240
26	888.5	47.8	354	2	I50237		Qy 241 ESNDENRMESKALFRITITYPWFQNSVILFLNKKDLLEEKIMSHLVDYFPEYDPO 300
27	887.5	47.7	354	2	S40509		Db 241 ESNDENRMESKALFRITITYPWFQNSVILFLNKKDLLEEKIMSHLVDYFPEYDPO 300
28	886.5	47.7	354	1	REHU02		Qy 301 DAWAREFTIKMVFIDLNPSDKIYIYSHFCATDENTIREVFAVAKDTIQLNKEYNLV 359
29	886.5	47.7	354	2	S28157		Db 301 DAQAREFTIKMVFIDLNPSDKIYIYSHFCATDENTIREVFAVAKDTIQLNKEYNLV 359

ALIGMENTS

DB 181 RVRVPPTGIEIYFPDLENIFRWDVGQCSRKRWICFENTVTSIMFLVASEYDQLV 240

Qy 241 ESDNENRMEESKALFRTITYPWQFONSSVILFLNKDLLEEKIMSHLVDFPEYDGPQR 300

Db 241 ESDNENRMEESKALFRTITYPWQFONSSVILFLNKDLLEEKIMSHLVDFPEYDGPQR 300

Qy 301 DAQAAREFLILKMFVLNPDSDKIIYSHFTCATDTENIRFVAAVKDTIQLNLKEYNLV 359

Db 301 DAQAAREFLILKMFVLNPDSDKIIYSHFTCATDTENIRFVAAVKDTIQLNLKEYNLV 359

RESULT 5

S45700 G-alpha-11 protein - African clawed frog

C;Species: *Xenopus laevis* (African clawed frog)

C;Accession: S45700

R;Shapiro, H.; Ray, J.; Lipinsky, D.; Oron, Y.; Battley, J.F.

F;BBS Lett. 348, 89-92, 1994

A;Title: Neuromedin B receptor, expressed in *Xenopus laevis* oocytes, selectively couples R;Reference number: S45699; MUID:94298961; PMID:8026589

A;Accession: S45700

A;Molecule type: mRNA

A;Residues: 1-359 <SHA>

A;Cross-references: PID:010494; NID:9505687; PID:AA52188.1; PID:9505688

C;Keywords: GTP binding; regulatory protein Gs alpha chain

F;46-53/Region: nucleotide-binding motif A (P-loop)

F;274-277/Region: GTP-binding NXKD motif

Query Match 90 4%; Score 1683; DB 1; Length 359;

Best Local Similarity 88.6%; Pred. No. 5.7e-14; Matches 318; Conservative 28; Mismatches 13; Indels 0; Gaps 0;

Matches 319; Conservative 25; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MTLESIMACCLSEPEAKARRINDEIERIVRDRDARERBLKLULGGESEGSKSNPKIQMR 60

Db 1 MTLESIMACCLSEPEAKARRINDEIERIVRDRDARERBLKLULGGESEGSKSNPKIQMR 60

Qy 61 IHHGSGISDEDKGKFTKLVQNYQFTAMQAMIRAMDTLKIPIYKPEHNAHAQLYREVDVEK 120

Db 1 MTLDSTMACCLSEPEAKESKRINAEKOLRDKKKDSRRLKPLKLUIGTGESGKSTPKIQMR 60

Qy 61 IHHGSGISDEDKGKFTKLVQNYQFTAMQAMIRAMDTLKIPIYKPEHNAHAQLYREVDVEK 120

Db 61 IHHGSGISDEDKGKFTKLVQNYQFTAMQAMIRAMDTLKIPIYKPEHNAHAQLYREVDVEK 120

Qy 121 VSAFENPVDAIKSLNDPGIQCEDCRREYQQLSDSTKYYINLDRVADAPYLPIQDVL 180

Db 121 VTFEIQYVNAIKTLWSDPGQECYDRRRQLQSAYVLTDVORIATVGYLPIQDVL 180

Qy 181 RVRVPPTGIEIYFPDLENIFRWDVGQCSRKRWICFENTVTSIMFLVASEYDQLV 240

Db 181 RVRVPPTGIEIYFPDLENIFRWDVGQCSRKRWICFENTVTSIMFLVASEYDQLV 240

Qy 241 ESDNENRMEESKALFRTITYPWQFONSSVILFLNKDLLEEKIMSHLVDFPEYDGPQR 300

Db 241 ESDNENRMEESKALFRTITYPWQFONSSVILFLNKDLLEEKIMSHLVDFPEYDGPQR 300

Qy 301 DAQAAREFLILKMFVLNPDSDKIIYSHFTCATDTENIRFVAAVKDTIQLNLKEYNLV 359

Db 301 DAQAAREFLILKMFVLNPDSDKIIYSHFTCATDTENIRFVAAVKDTIQLNLKEYNLV 359

RESULT 6

RGM511 GTP-binding regulatory protein G11 alpha chain - mouse

N;Alternate names: guanine nucleotide binding protein G11 alpha chain; heterotrimeric G

C;Species: *Mus musculus* (house mouse)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001

C;Accession: B38414

R;Strathmann, M.; Simon, M.I.

Proc. Natl. Acad. Sci. U.S.A. 87, 9113-9117, 1990

A;Title: G protein diversity: a distinct class of alpha subunits is present in vertebrates

A;Reference number: A38414; MUID:91067657; PMID:2123549

A;Accession: B38414

A;Molecule type: mRNA

Query Match 90 4%; Score 1683; DB 1; Length 359;

Best Local Similarity 89.1%; Pred. No. 6.7e-14; Matches 320; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

Matches 320; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

A;Residues: 1-359 <STR>

A;Cross-references: GB:W55411; NID:919499; PID:9193505.1; PID:9193500

C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that re

ains. The beta and gamma chains, required for GTPase activity, appear to be common to

all. It is specific for each type of G protein.

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transductio

F;46-53/Region: nucleotide-binding motif A (P-loop)

F;274-277/Region: GTP-binding NXKD motif

F;52/Binding site: GTP (Lys) #status predicted

F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 90 4%; Score 1683; DB 1; Length 359;

Best Local Similarity 89.1%; Pred. No. 6.7e-14; Matches 320; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

Matches 320; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

A;Residues: 1-359 <STR>

A;Cross-references: GDB:132587; OMIM:139313

A;Map position: 19p13.3-19p13.3

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transductio

F;46-53/Region: nucleotide-binding motif A (P-loop)

F;274-277/Region: GTP-binding NXKD motif

F;52/Binding site: GTP (Lys) #status predicted

F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 90 4%; Score 1683; DB 1; Length 359;

Best Local Similarity 89.1%; Pred. No. 6.7e-14; Matches 320; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

Matches 320; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

A;Residues: 1-359 <STR>

A;Cross-references: GB:W55411; NID:919499; PID:9193505.1; PID:9193500

C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that re

ains. The beta and gamma chains, required for GTPase activity, appear to be common to

all. It is specific for each type of G protein.

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transductio

F;46-53/Region: nucleotide-binding motif A (P-loop)

F;274-277/Region: GTP-binding NXKD motif

F;52/Binding site: GTP (Lys) #status predicted

F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

A;Residues: 217-267 <STR>
 A;Cross-references: GB:M57616; NID:919380; PIDN:AAA63304.1; PID:9193381; GB:M26739
 C;Superfamily: GTP-binding regulatory protein Gs alpha chain
 C;Keywords: GTP binding; nucleotide binding; P-loop
 F;42-49/Region: nucleotide-binding motif A (P-loop)
 F;152-154/Region: GTP-binding SAKL motif
 F;270-273/Region: GTP-binding NKXD motif

Query Match 82.5%; Score 1535; DB 2; Length 355;
 Best Local Similarity 82.1%; Pred. No. 2.3e-103;
 Matches 288; Conservative 35; Mismatches 28; Indels 0; Gaps 0;
 QY 9 CCLSLREKEKSERISERIEERHVRDRDKARRELKLILLGTEGSGKSTFIKOMRIGHSGYS 68
 5 CCLSLREKEKSERISERIEERHVRDRDKARRELKLILLGTEGSGKSTFIKOMRIGHSGYS 64

QY 69 DEDKGKFTKLYQVQNTTAMQAMIRAMDTLKPYKEHNKAHQLYTREDEVKSAFNPY 128
 65 DEDKGKFTKLYQVQNTTAMQAMIRAMDTLKPYKEHNKAHQLYTREDEVKSAFNPY 128

Db 129 VDAIKSLWNPDQPGIQECYCDRREIQQLSDSTKYLNDLDRDPALEYTQDQLVRLVRVPTG 188
 QY 125 VAAIKQLWLDPGICQCYCDRREIQQLSDAKYVTLDRDPALEYTQDQLVRLVRVPTG 184

Db 189 IIEYFPDQSVIFRMDVGQSRERKWKHCFENVTMFLVALSEYDQVLMRDNRM 248
 185 IIEYFPDLENLIFRMDVGQSRERKWKHCFENVTMFLVALSEYDQVLMRDNRM 244

Db 249 ESKALFRTITYPWFQNSVTLFLNKDLLEEKIMSHVYDVFPEYDGFQDAGAREF 308

QY 245 ESKALFRTITYPWFQNSVTLFLNKDLLEEKIMSHVYDVFPEYDGFQDAGAREF 304

QY 309 ILMKMDVLNPSDKTLYSHTCATTELENTRFVAAVKDTIQLQNLKEYNLV 359

Db 305 IILKLYQDQNDPDKERKVYSHFTCATDTELENTRFVAAVKDTIQLQNLKEYNLV 355

RESULT 11
 S34/47 GTP-binding regulatory protein Gq alpha chain - great pond snail
 C;Species: Lymnaea stagnalis (great pond snail)

C;Accession: S65461; SL4347
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Feb-2001

Db 1 R;Khol, J.C.; Rammatsingh, S.; van Kesteren, E.R.; van Minnen, J.; Planta, R.J.; van Hee, Eur. J. Biochem. 230, 193-199, 1995
 A;Title: Cloning of a molluscan G protein alpha subunit of the Gq class which is expressed in A;Reference number: S65461; MUID:95324523; PMID:7601100

A;Accession: S65461
 A;Molecule type: mrNA
 A;Residues: 1-355 <RNO>

Db 2 C;superfamily: GTP-binding regulatory protein Gs alpha chain - great pond snail
 C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transduction

F;150-152/Region: nucleotide-binding motif A (P-loop)

F;268-271/Region: GTP-binding NKXD motif

F;46/Binding site: GTP (Lys) #status predicted

F;177/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 81.9%; Score 1524; DB 2; Length 353;
 Best Local Similarity 81.6%; Pred. No. 1.4e-102;
 Matches 288; Conservative 29; Mismatches 36; Indels 0; Gaps 0;
 QY 7 MACCLSLREKEKSERINDEIERHVRDRDKARRELKLILLGTEGSGKSTFIKOMRITHGSG 66
 Db 1 MACCLSLREKEKSERINDEIERHVRDRDKARRELKLILLGTEGSGKSTFIKOMRIGHGQ 60

QY 67 YSDEDKGKFTKLYQVQNTTAMQAMIRAMDTLKPYKEHNKAHQLYTREDEVKSAFNPY 124
 Db 61 YSEEDKRAHTRLVYQNTTAMQAMIRAMDTLKPYKEHNKAHQLYTREDEVKSAFNPY 120

QY 125 ENPYDAIKSLWNPDQPGIQECYCDRREIQQLSDSTKYLNDLDRDPALEYTQDQLVRLVRVPTG 184
 Db 121 EPPYVSIKELWEDSGIQECYCDRREIQQLSDAKYVTLDRDPALEYTQDQLVRLVRVPTG 180

QY 185 PTGTCIIEYFPDQSVIFRMDVGQSRERKWKHCFENVTMFLVALSEYDQVLMRDNRM 244

Db 181 PTGTCIIEYFPDQSVIFRMDVGQSRERKWKHCFENVTMFLVALSEYDQVLMRDNRM 240

QY 245 ERMEESKALFRTITYPWFQNSVTLFLNKDLLEEKIMSHVYDVFPEYDGFQDAGAREF 308

Db 241 ERMEESKALFRTITYPWFQNSVTLFLNKDLLEEKIMSHVYDVFPEYDGFQDAGAREF 300

Db 305 AREFIKLMFDLNPDSKTIYSHFTCATTELENTRFVAAVKDTIQLQNLKEYNLV 359
 301 AREFIKLMFDLNPDAKTIYSHFTCATTELENTRFVAAVKDTIQLQNLKEYNLV 355

RESULT 13
 S33/309 GTP-binding regulatory protein Gq alpha chain - northern European squid
 C;Species: Loligo forbesi (northern European squid)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Feb-2001
 C;Accession: S33309
 R;Ryba, N.J.P.; Findlay, J.B.C.; Reid, J.D.

QY 67 YSDEDKGKFTKLYQVQNTTAMQAMIRAMDTLKPYKEHNKAHQLYTREDEVKSAFNPY 126
 61 YSDEDKRSHTRKIVYQNTFMANHAMHMRAMDTNQYINPAKRENGNMIRQDYEVTMFTD 120

Db 127 PYVDAIKSLWNPDQPGIQECYCDRREIQQLSDAKYVTLDRDPALEYTQDQLVRLVRVPTG 186

Db 1 MACCIPDEKLEQKRINQETEEROLKKDRDKARRELKLILLGTEGSGKSTFIKOMRIGHGAG 60

BioChem: J 292: 333-341 (1993)
 A; Reference number: S33309; MUID: 93277493; PMID: 8503868
 A; Accession: S33309
 A; Status: Preliminary
 A; Molecule type: mRNA
 A; Residues: 1-354 <RYB>
 A; Cross-references: EMBL: L10289
 C; Superfamily: GTP-binding regulatory protein Gs alpha chain
 C; Keywords: GTP binding; nucleotide binding; P-loop
 F; 40-47/Region: nucleotide-binding motif A (P-loop)
 F; 150-152/Region: GTP-binding SAK/L motif
 F; 269-272/Region: GTP-binding NKA motif

 Query Match 79.0%; Score 1469.5; DB 2; Length 354;
 Best Local Similarity 77.4%; Pred. No. 1.2e-98;
 Matches 274; Conservative 39; Mismatches 40; Indels 1; Gaps 1;

 QY 7 MACCLSEEAKEARRINDETERHVRDKDRARREKKLLIGTGESKRSTFKOMRITHGSG 66
 Db 1 MACCLSEEAKEARRINDETERHVRDKDRARREKKLLIGTGESKRSTFKOMRITHGSG 60

 QY 67 YSEDEDKRKGFTKLKYQNYNITFAMQAMIRAMOTLKKIPKYKHEHKAHQALVREYDVEKSAFEN 126
 Db 61 YSEBEDRKGFKEVYQNYNIFSAIQTLIAAMENTSLEYKDPSNNEHAFLNSIDADSADIFED 120

 QY 127 PYVDAIKSIWNDPGIQCYDQRRTYQLSUDSTKYLNDLDRVADPAKLPQDODVLRVPT 186
 Db 121 GHVTAIKCGCTWDPGMOCYDQRREYQDLSAKYVDDVERIHEPGCYIPTQDILVRVPT 180

 QY 187 TGTYIEPPDLSQVTFRMDVGGQESERRWIKHCENNTSMFLVYALSEYDQVLSND-E 245
 Db 181 TGTYIEPPDLSITFMRMDVGGQESERRWIKHCENNTSMFLVYALSEYDQVLSND-E 240

 QY 246 NRMEESKALFRTITYPWNFONSSVTLFLNKNDLKEKIMSHLVYVPEPDGQDQAQA 305
 Db 241 NRMEESKALFRTITYPWNFONSSVTLFLNKNDLKEKIMSHLADDFPDYDGPKDYEAA 300

 QY 306 REPIKAKMVDLNDPSDKIYSHFICATDENTIREVFAAKDTIQLNLKYNYLV 359
 Db 301 REPMDSYMDLNEDKMLYYHICATDENTIREVFAAKDTIQLNLKYNYLV 354

RESULT 14
 JN0115 GTP-binding regulatory protein dgq alpha chain - fruit fly (Drosophila melanogaster)
 N; Alternate names: dgq protein
 C; Species: Drosophila melanogaster
 C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Feb-2001
 C; Accession: JN0115
 R; Lee, Y.-J.; Dobbs, M.B.; Verardi, M.L.; Hyde, D.R.
 Neuron 5, 889-898, 1990
 A; Title: dgq, a drosophila gene encoding a visual system-specific G alpha molecule.
 A; Reference number: JN0115; MUID: 91097801; PMID: 2125225
 A; Accession: JN0115
 A; Molecule type: DNA
 A; Residues: 1-360 <LEE>
 C; Genetics:
 A; Gene: dgq
 A; Cross-references: FlyBase:FBgn0004435
 A; Introns: 40/1; 101/3; 155/2; 196/2; 239/3; 298/1; 334/1
 C; Superfamily: GTP-binding regulatory protein Gs alpha chain
 C; Keywords: alternative splicing; GTP binding; nucleotide binding; P-loop
 F; 1-350/Product: GTP-binding regulatory protein dgq alpha chain I #status Predicted <MAT>
 F; 1-297; 333-360/Product: GTP-binding regulatory protein dgq alpha chain II #status Predicted <MAT>
 F; 40-47/Region: nucleotide-binding motif A (P-loop)
 F; 150-152/Region: GTP-binding SAK/L motif
 F; 269-272/Region: GTP-binding NKA motif

Tue Jul 1 09:54:47 2003

us-09-899-295-2.rpr

Page 7

QY 358 LV 359
|:
Db 373 LL 374

Search completed: June 30, 2003, 16:18:23
Job time : 20 secs



RL BIOL. Psychiatry 32:549-579(1992).
 RN [3]
 RP SEQUENCE OF 238-331 FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Kidney cortex;
 RA Thomas C.P.;
 RT "GTP-binding protein expression in glomerular mesangial cells.";
 RI Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.
 CC -I- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
 CC -I- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 DR EMBL; AF234260; RAAF9930_1; ALT_INIT.
 DR HSSP; P10824; 150F.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR PRAM; PF00503; G-alpha; 1.
 DR prodom; PDD00281; Gprotein_alpha; 1.
 DR SMART; SM00275; G-alpha; 1.
 DR GRIP-binding; Transducer; Multigene family: ADP-ribosylation;
 KW Palmitate; Lipoprotein.
 FT LIPID 3 3
 FT LIPID 4 4
 FT NP_BIND 40 47
 FT NP_BIND 199 203
 FT NP_BIND 268 271
 FT MOD_RES 177 177
 FT CONFLICT 85 85
 FT SEQUENCE 353 AA; 41469 MW; BB4C211FDD47534;
 Query Match 97.7%; Score 1818; DB 1; Length 353;
 Best Local Similarity 98.9%; Pred. No. 2e-129; DB 1; Length 349;
 Matches 349; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 OV 7 MACCLSERAEKAERNINDEIERHVRDKDARRELKLKLIGTGESKGKFPIKOMRITHGSG 66
 DB 1 MACCLSERAEKAERNINDEIERHVRDKDARRELKLKLIGTGESKGKFPIKOMRITHGSG 60
 QY 67 YSDPEDKRFTKLYQONITFAMQMTRANDTLPKPYKEHNKAHQLYREVDEYKSAFEN 126
 DB 61 YSDPEDKRFTKLYQONITFAMQMTRANDTLPKPYKEHNKAHQLYREVDEYKSAFEN 120
 QY 127 PYDAIKSLWNDPGIQECDYDRREYQIQLSDSTKYLNDLDRDPAVLPFTQDVLVRVPT 186
 DB 121 PYDAIKSLWNDPGIQECDYDRREYQIQLSDSTKYLNDLDRDPAVLPFTQDVLVRVPT 180
 QY 187 TGIEYPPDQLQSVIFRMVYDGGORSERKRWKHFENYVSMFLVMSBYDQVILVESDEN 246
 DB 181 TGIEYPPDQLQSVIFRMVYDGGORSERKRWKHFENYVSMFLVMSBYDQVILVESDEN 240
 QY 247 RMEESKALFRTIITYPWFQNSVYTFELNKDKLLEEKINMYSHVLYDFEPYDGPDAQAR 306
 DB 241 RMEESKALFRTIITYPWFQNSVYTFELNKDKLLEEKINMYSHVLYDFEPYDGPDAQAR 300
 QY 307 EFLKMFEDLNPDSKTYSHFCATDENTIRYFAAKVDTIQLNKEYNL 359
 DB 301 EFLKMFEDLNPDSKTYSHFCATDENTIRYFAAKVDTIQLNKEYNL 353
 RESULT 4
 GPO_HUMAN ID GBQ_HUMAN STANDARD; PRT; 353 AA.

AC P50148; 013462; 092471; 015108;
 DT 01-OCT-1996 (Rel. 34; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Guanine nucleotide-binding protein G(q), alpha subunit.
 RN GNQ OR GAO.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9623032; PubMed=8825633;
 RA doing Q., Shenker A., Way J., Haddad B.R., Lin K., Hughes M.R.,
 RA McBride W.O., Spiegel A.M., Bartley J.;
 RT "Molecular cloning of human G alpha q cDNA and chromosomal
 RT localization of the G alpha q gene (GNAQ) and a processed
 RT pseudogene.";
 RL Genomics 30:470-475(1995).
 [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=prostate;
 RA MEDLINE=96256639; PubMed=88664309;
 RA "Human G(alpha q): cDNA and tissue distribution.";
 RL Biochim. Biophys. Acta 1281:125-128(1996).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96433124; PubMed=8836152;
 RA Johnson G.J., Leis L.A., Dunlop P.C.,
 RT "Specificity of G alpha q and G alpha 11 gene expression in platelets
 RT and erythrocytes. Expressions of cellular differentiation and species
 RT differences";
 RL Biochem. J. 318:1023-1031(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Bai X.H., Acharya R., Rivera C., Murtagh J.J.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 74-229 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=93081611; PubMed=1333286;
 RA Lesch K.-P., Manji H.K.;
 RT "Signal-transducing G Proteins and antidepressant drugs: evidence for
 RT modulation of alpha subunit gene expression in rat brain.";
 RL Biol. Psychiatry 32:549-575(1992).
 RN [6]
 RP SEQUENCE OF 238-331 FROM N.A.
 RC TISSUE=Hematopoietic;
 RX MEDLINE=9607138; PubMed=7492305;
 RA Thomas C.P., Dunn M.J., Mattera R.;
 RT "Ca2+ signalling in K562 human erythroleukaemia cells: effect of
 RT dimethyl sulphoxide and role of G-proteins in thrombin- and
 RT thromboxane A2-activated pathways.";
 RL Biochem. J. 312:151-158(1995).
 CC -I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.
 CC -I- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
 CC -I- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN OVARY, PROSTATE,
 CC TESTIS AND COLON.
 CC -I- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
 CC
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 CC
 DR EMBL; U40038; AAC50363_1; ALT_INIT.

DR	EMBL; U43083; AAB06375.1; ALT_INIT.	RN	[1]
DR	L76256; AAB39981; ALT_INIT.	RP	SEQUENCE FROM N.A.
DR	EMBL; AFO11496; AAB043011; ALT_INIT.	RA	RN
DR	HSSP; P10824; IBOF.	RL	Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
DR	Genew; HGNC; 4390; GNAQ.	RN	[2]
DR	MIM; 600918; -.	RP	SEQUENCE FROM N.A.
DR	InterPro; IPR001019; Gprotein_alpha.	RC	TISSUE="oocyte";
DR	Pfam; PF00503; G-alpha; 1.	RX	MEDLINE=94298961; Pubmed=8025589;
DR	PRINTS; PRO0318; GproteinINA.	RA	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
DR	ProDom; P000281; Gprotein_alpha; 1.	RL	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
DR	SMART; SM00275; G-alpha; 1.	RT	FEBs Lett. 348:89-92(1994).
KW	GTP-binding; Transducer; Multigene family; ADP-ribosylation;	RN	[3]
FT	Palmitate; Lipoprotein.	RP	ERRATUM.
FT	LIPID 3 3	RA	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
FT	LIPID 4 4	RL	FEBs Lett. 349:318-318(1994).
FT	NP_BIND 40 47	CC	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
FT	NP_BIND 199 203	CC	SEQUENCE FROM N.A.
FT	NP_BIND 268 271	CC	TISSUE="oocyte";
FT	MOD_RES 177 177	CC	MEDLINE=94298961; Pubmed=8025589;
FT	MOD_RES 177 177	RA	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
FT	CONFFLICT 22 23	RL	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
FT	CONFFLICT 86 86	CC	SEQUENCE FROM N.A.
FT	CONFFLICT 97 97	CC	TISSUE="oocyte";
FT	CONFFLICT 165 165	CC	MEDLINE=94298961; Pubmed=8025589;
FT	CONFFLICT 318 318	RA	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
FT	CONFFLICT 331 331	RL	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
FT	CONFFLICT 352 352	CC	SEQUENCE FROM N.A.
FT	SEQUENCE 353 AA; 41425 MW; E7798E07B1F4904C CRC64;	CC	TISSUE="oocyte";
Query Match	97 %; Score 1817; DB 1; Length 353;	CC	MEDLINE=94298961; Pubmed=8025589;
Best Local Similarity	99 %;	CC	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
Matches	350; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	CC	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
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QY	67 YSDEDRKGFTKLVYONIFTAMOAMTRAMDTIKIPKYEHINKHAQOLVREVDVKEVSAFEN 126	CC	MEDLINE=94298961; Pubmed=8025589;
Db	61 YSDEDRKGFTKLVYONIFTAMOAMTRAMDTIKIPKYEHINKHAQOLVREVDVKEVSAFEN 120	CC	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
QY	127 PYDAIKSLANDPGIQCYVRRREYQLSDSKYYLNDLQVADPYLPTQDVLVRVPT 186	CC	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
Db	121 PYDAIKSLANDPGIQCYDPRREYQLSDSKYYLNDLQVADPYLPTQDVLVRVPT 180	CC	SEQUENCE FROM N.A.
QY	187 TGIEYPFDIQSIVFRMVDVGGQRSERRKWHCFENVTSMFLValseyQDVLVSEVDNEN 246	CC	TISSUE="oocyte";
Db	181 TGIEYPFDIQSIVFRMVDVGGQRSERRKWHCFENVTSMFLValseyQDVLVSEVDNEN 240	CC	MEDLINE=94298961; Pubmed=8025589;
QY	247 RMEESKALFRITITYWFFONSVILFLNKKDLEKIMYHLDVYPEYQGPQDQAAR 306	CC	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
Db	241 RMEESKALFRITITYWFFONSVILFLNKKDLEKIMYHLDVYPEYQGPQDQAAR 300	CC	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
QY	307 EFLKNEVDIINPSDKIYSHFTCATDTENIREVAKTIQIQLNKENY 359	CC	SEQUENCE FROM N.A.
Db	301 EFLKNEVDIINPSDKIYSHFTCATDTENIREVAKTIQIQLNKENY 353	CC	TISSUE="oocyte";
RESULT 5		CC	MEDLINE=94298961; Pubmed=8025589;
GBO_XENLA	STANDARD; PRT; 353 AA.	CC	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
ID		CC	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
AC	P38410;	CC	SEQUENCE FROM N.A.
DT	01-OCT-1994 (Rel. 30, Created)	CC	TISSUE="oocyte";
DT	01-OCT-1994 (Rel. 30, Last sequence update)	CC	MEDLINE=94298961; Pubmed=8025589;
DT	16-OCT-2001 (Rel. 40, Last annotation update)	CC	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
DE	Guanine nucleotide-binding protein G(q), alpha subunit.	CC	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
GN	GNAQ.	CC	SEQUENCE FROM N.A.
OS	Xenopus laevis (African clawed frog).	CC	TISSUE="oocyte";
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CC	MEDLINE=94298961; Pubmed=8025589;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipida;	CC	Shapiro H., Way J., Lipinsky D., Oron Y., Battye J.F.;
OC	Xenopoda; Xenopidae; Xenopus.	CC	"Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples to G alpha q and not G alpha 11.";
NCBI_TaxID=8355;		CC	SEQUENCE FROM N.A.

QY	247	RMEKSALKFRTITYPWFQNSVILFLNKDKLLEEKIMYSHLVDPEYDGPORDAAR	306
Db	301	EFILKMFVLDNPSDKIYSHFTCATDENTIRFVAAVKDTIQLNLKEYNLV	359
QY	307	EFILKMFVLDNPSDKIYSHFTCATDENTIRFVAAVKDTIQLNLKEYNLV	359
Db	301	EFILKMFVLDNPSDKIYSHFTCATDENTIRFVAAVKDTIQLNLKEYNLV	353
RESULT 6			
GB11_MELGA	ID	GB11_MELGA	STANDARD;
AC	P45645;	PRT;	359 AA.
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
RT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Guanine nucleotide-binding protein, alpha-11 subunit.		
GN	GNAL1.		
OS	Meleagris gallopavo (Common turkey).		
RC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;		
RA	Archaeozoa; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.		
OX	NCBI_TaxID=9103;		
RN	[1]		
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE:93207527; PubMed:8457205;		
RA	Maurice D.H., Waldo G.L., Morris A.J., Nicholas R.A., Harden T.K.;		
RT	Identification of G alpha 11 as the phospholipase C-activating G-protein of turkey erythrocytes.;		
RT	biochem. J. 290:765-770(1993).		
CC	-I- FUNCTION: guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane signaling systems. ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C.		
CC	-I- SUBUNIT: G proteins are composed of 3 units (ALPHA, BETA & GAMMA).		
CC	THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.		
CC	-I- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (GQ).		
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CC	-----		
CC	EMBL; X37072; CAA51530.1; -.		
CC	DR HSSP; P10824; IBOF.		
CC	DR Pfam; PF00503; G-alpha; 1.		
CC	DR PRINTS; PR00318; GPROTEINA.		
CC	DR PRODOM; P000281; Gprotein_alpha; 1.		
CC	DR SMART; SM00275; G-alpha; 1.		
CC	DR GTP-binding; Transducer; Multigene family; ADP-ribosylation.		
CC	FT NP_BIND; 46 53 GTP (BY SIMILARITY).		
CC	FT NP_BIND; 205 209 GTP (BY SIMILARITY).		
CC	FT NP_BIND; 274 277 GTP (BY SIMILARITY).		
CC	FT MOD_RES; 183 183 ADP-RIBOSYL[1] (BY ACTION OF CTX)		
CC	FT SEQUENCE 359 AA; 42058 MW; B9E16427169BEIAE CRC64;		
CC	-----		
CC	Query Match 91.9%; score 1709; DB 1; Length 359;		
CC	Best Local Similarity 90.3%; Pred. No. 3.1e-121; Matches 324; Conservative 22; Mismatches 13; Indels 0; Gaps 0;		
CC	-----		
QY	1	W1LESMACCLSEEAKARRNDEIERRVDRKDRARRELKLILLGCGESGKSTFIKOMR	60
Db	1	W1LESMACCLSEEAKARRNDEIERRVDRKDRARRELKLILLGCGESGKSTFIKOMR	60
QY	61	IIHGS3YSDDEDKRGFKFLKVQNTAMTRAMDTKPYKVENKHAOLYPREVDVEK	120
Db	61	IIHGS3YSDDEDKRGFKFLKVQNTAMTRAMDTKPYKVENKHAOLYPREVDVEK	120
RESULT 7			
GB11_BOVIN	ID	GB11_BOVIN	STANDARD;
AC	P38409;	PRT;	359 AA.
DT	01-OCT-1994 (Rel. 30, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Guanine nucleotide-binding protein, alpha-11 subunit (G11).		
GN	GNAL1.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
OC	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:91286503; PubMed:1905731;		
RA	Nakamura F., Ogata K., Shiozaki K., Kaneyama K., Ohara K., Haga T.,		
RA	Nukeda T.,		
RT	"Identification of two novel GTP-binding protein alpha-subunits that lack apparent ADP-ribosylation sites for pertussis toxin".		
RL	J. Biol. Chem. 266:12676-12681(1991).		
CC	-I- FUNCTION: guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane signaling systems.		
CC	-I- SUBUNIT: G proteins are composed of 3 units (ALPHA, BETA & GAMMA).		
CC	THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.		
CC	-I- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (GQ).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; D90336; BAA4350.1; ALT-INIT.		
CC	DR PIR; B40891; B40891.		
CC	DR HSSP; P10824; IBOF.		
CC	DR InterPro; IPR001019; Gprotein_alpha.		
CC	DR Pfam; PF00503; G-alpha; 1.		
CC	DR PRINTS; PR00318; GPROTEINA.		
CC	DR PRODOM; P000281; Gprotein_alpha; 1.		
CC	DR SMART; SM00275; G-alpha; 1.		
CC	GTP-binding; Transducer; Multigene family; ADP-ribosylation.		
CC	FT NP_BIND; 46 53 GTP (BY SIMILARITY).		
CC	FT NP_BIND; 205 209 GTP (BY SIMILARITY).		
CC	FT NP_BIND; 274 277 GTP (BY SIMILARITY).		
CC	FT MOD_RES; 183 183 ADP-RIBOSYL[1] (BY ACTION OF CTX)		
CC	FT SEQUENCE 359 AA; 42070 MW; B0BAC4FB5AE8D5 CRC64;		
CC	-----		
CC	Query Match 90.9%; score 1691; DB 1; Length 359;		
CC	Best Local Similarity 89.4%; Pred. No. 6.9e-120;		

DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Guanine nucleotide-binding protein, alpha-11 subunit.
 GN GNA11
 OS *Xenopus laevis* (African clawed frog).
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Chondrocephala; Vertebrata; Euteleostomi; Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1] SEQUENCE FROM N.A.
 RQ TISSUE=Oocyte;
 RX MEDLINE=94298661; PubMed=8026589;
 RA Shapira H., Way J., Lipinsky D., Oron Y., Battley J.F.;
 RT "Neuromedin B receptor expressed in *Xenopus laevis* oocytes, selectively couples to G alpha q and not G alpha 11.";
 RL FEBS Lett. 348:89-92(1994).
 RN [2] ERRATUM.
 RA Shapira H., Way J., Lipinsky D., Oron Y., Battley J.F.;
 RL FEBs Lett. 349:318-318(1994).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
 CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
 CC
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 CC
 DR EMBL; U10494; AAA52188.1; -.
 DR HSSP; PI0824; -.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR PFM; PR0053; G-alpha; 1.
 DR PRINTS; PR00318; GPROTEINA.
 DR Problem; PD00281; Gprotein_alpha; 1.
 DR SMART; SM00275; G-alpha; 1.
 DR SMART; SM00275; G-alpha; 1; Multigene family; ADP-ribosylation.
 FT KW GTP-binding; Transducer; Multigene family; ADP-ribosylation.
 FT NP_BIND 46 53 GTP (BY SIMILARITY).
 FT NP_BIND 205 209 GTP (BY SIMILARITY).
 FT NP_BIND 274 277 GTP (BY SIMILARITY).
 FT MOD_RES 183 183 ADP-RIBOSYL[1] (BY ACTION OF CTX) (BY FT SIMILARITY).
 SQ SEQUENCE 359 AA; 42088 MW; DAB37693FDDB70 CRC64;
 CC
 CC Query Match 90.6%; Score 1685; DB 1; Length 359;
 CC Best Local Similarity 88.9%; Pred. No. 1. 9e-19;
 CC Matches 319; Conservative 25; Mismatches 15; Indels 0; Gaps 0;
 CC
 CC 1 MTLESIMACCLSEEAKEARRINDETERHVRDRKDRDARREKLRLLLGTGESGKSTIKQMR 60
 CC 1 |||:|||||:|||||:||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 DB 1 MTLDSMCCULSEEVKEKRINAELEKQLRDRKDKDSRREKLRLLLGTGESGKSTIKQMR 60
 CC
 CC 61 LIHGSYSKEDDKRGFKTKLVIQNIIFTAMQAMTRAMDTLKIPIKYEHNAHQALQREVDEK 120
 CC 61 LIHGSYSKEDDKRGFKTKLVIQNIIFTAMQAMTRAMDTLKIPIKYEHNAHQALQREVDEK 120
 CC
 CC 121 VSAFENPYDIAKSLWDPGIOCYDRREYQLSDTKYYLNDLQRYDAFLYLPQDQDVL 180
 CC 121 VCTFEPYVNAIKNLMQDPLQESTKYYLNDLQRYDAFLYLPQDQDVL 180
 CC
 CC 181 RVRVPPTGIEYPFDLQSVFIRMVYGGQSRERRKWIHCFENVTSIMPLVALSEDQVLV 240
 CC 181 |||:|||||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 DB 181 RVRVPPTGIEYPFDLQSVFIRMVYGGQSRERRKWIHCFENVTSIMPLVALSEDQVLV 240
 CC
 CC 241 ESDNENRMEESKALFRITITYFWFQNSSVILFLNKKDLERKIMSHLVDFPEXDGPQR 300
 CC |||:|||||:|||||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 CC
 DB 241 ESDNENRMEESKALFRITITYFWFQNSSVILFLNKKDLERKIMSHLVDFPEXDGPQR 300
 CC
 CC GB1_MOUSE
 CC ID GB1_MOUSE . STANDARD; PRT; 359 AA.
 CC AC P21278; Q61939; -.
 CC DT 01-MAY-1991 (Rel. 18, last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, last annotation update)
 CC DE Guanine nucleotide-binding protein, alpha-11 subunit.
 CC GN GNA11 OR GNA-11.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OC NCBI_TaxID=10090;
 CC RN [1] SEQUENCE FROM N.A.
 CC RQ
 CC RX MEDLINE=9106757; PubMed=2123549;
 CC RA Strathmann M.; Simon M.I.;
 CC RT "G protein diversity: a distinct class of alpha subunits is present in vertebrates and invertebrates.";
 CC RT Proc. Natl. Acad. Sci. U.S.A. 87:9113-9117(1990).
 CC RN [2] SEQUENCE FROM N.A.
 CC RQ STRAIN=129/SV;
 CC RX MEDLINE=96435432; PubMed=8838318;
 CC RA Davignon I.; Bernard M.; Gavrilova O.; Sweet K.; Wilkie T.M.;
 CC "Gene structure of murine Gna11: tandemly duplicated Gq class G protein alpha subunit genes.";
 CC RL Genomics 31:359-366(1995).
 CC RN [3] SEQUENCE OF 211-271 FROM N.A.
 CC RX MEDLINE=9001788; PubMed=250088;
 CC RA Strathmann M.; Wilkie T.M.; Simon M.I.;
 CC "Diversity of the G-protein family: sequences from five additional alpha subunits in the mouse";
 CC RT Proc. Natl. Acad. Sci. U.S.A. 86:7407-7409(1989).
 CC CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C.
 CC CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
 CC CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
 CC
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 CC
 CC 1 EMBL; M55411; AAA63305.1; -.
 CC EMBL; U37413; AAB36839.1; -.
 CC EMBL; U37411; AAB36839.1; JOINED.
 CC EMBL; U37412; AAB36839.1; JOINED.
 CC EMBL; M57617; AAA63301.1; -.
 CC PIR; B38434; R0MS11.
 CC HSSP; P10824; 1BOF.
 CC DR MGD; MGII:9766; Gna11.
 CC InterPro; IPR001019; Gprotein_alpha.
 CC PFM; PF0050; G-alpha; 1.
 CC PRINTS; PR00318; GPROTEINA.
 CC Problem; PD00281; Gprotein_alpha; 1.
 CC SMART; SM00275; G-alpha; 1; Multigene family; ADP-ribosylation.
 CC NP_BIND 46 53 GTP (BY SIMILARITY).

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DR EMBL; D90335; BAA14349.1; - .

DR PIR; A40891; A40891.

DR HSSP; P10824; IBOF.

DR InterP; IPR001019; Gprotein_alpha.

DR Pfam; PF00503; G-alpha; 1.

DR PRINTS; PR00318; Gprotein_alpha.

DR PRODom; P000281; Gprotein_alpha; 1.

DR SMART; SM00275; G-alpha; 1.

KW GTP-binding; transducer; Multigene family; ADP-ribosylation.

FT NP_BIND 42 49 GTP (BY SIMILARITY).

FT NP_BIND 201 205 GTP (BY SIMILARITY).

FT NP_BIND 270 273 GTP (BY SIMILARITY).

FT MOD_RES 179 179 ADP-RIBOSYL[1] (BY ACTION OF Cpx) (BY SIMILARITY).

FT SEQUENCE 355 AA; 41498 MW; 60888CC6C9B7243B CRC64;

Query Match 82.7%; Score 13.38; DB 1; Length 355;
 Best Local Similarity 82.3%; Pred. No. 2. 1e-108; Mismatches 29; Indels 0; Gaps 0;

Matches 289; Conservative 33; Mismatches 29; Indels 0; Gaps 0;

Qy 9 CCLSEEEAKEARRINDELETERHYRDKDRARRELKLLLTGSGSKSFPIKOMRIIHGSYS 68

Db 5 CCLSAEEKKESQRISAEERQRLRDKDARRELKLLLTGSGSKSFPIKOMRIIHGSYS 64

Qy 69 DEDRKRGFTKLVQNFQAMIRAMDTLQVYCVQENKAQMLTREVKVSTLSRDQ 124

Db 65 DEDRKRGFTKLVQNFQAMIRAMDTLQVYCVQENKAQMLTREVKVSTLSRDQ 124

Qy 129 VDAIKS1WNPQIQCYDRREYQLDSTSKYLNDLDRRAVPAYLPTQDYLVRVPTG 188

Db 125 VEAIKQWQDQPGTOECYDRREYQLDSTSKYLNDLDRRAVPAYLPTQDYLVRVPTG 184

Qy 189 IIEYPFDLQSVFMRMVQGQSERRKWICFENVTSMFLVSEYDQVLVSEEDNENRM 248

Db 185 IIEYPFDLLENIFRMDVGGQSERRKWICFENVTSMFLVSEYDQVLVSEEDNENRM 244

Qy 249 EESKAFLRTITYPWFQNSVILFLNKDLIEEKIMSHLYDYPEPDGPORDAQAREF 308

Db 245 EESKAFLRTITYPWFQNSVILFLNKDLIEEKIMSHLYDYPEPDGPORDAQAREF 304

Qy 309 IILKMFVLDLNPDSKDKIYSHFCATDTENIREVFAAVKDTIQLQNLREFNLV 359

Db 305 IILKLYQDQNPDKREKVYSHFTCATDTENIREVFAAVKDTIQLQNLREFNLV 355

RESULT 13

GB14_XENLA STANDARD; PRT; 354 AA.

AC 073819; 073819; 073819;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Guanine nucleotide-binding protein, alpha-14 subunit.

GN GNA14.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

OC Xenopodinae; Xenopus.

NCBI_TaxID=8355;

[1] SEQUENCE FROM N.A.

RX MEDLINE=98344029; PubMed=9677362;

RA Shapira H., Amit I., Revach M., Oron Y., Battey J. F.;

RT "Galphi14 and Galphiq mediate the response to trypsin in Xenopus oocytes.";

RL J. Biol. Chem. 273:19431-19436(1998);

J. FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE

CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C.

CC MEDIATES RESPONSES TO TRYPSIN.

-1- SUBUNITS: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).

CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.

CC -1- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY SUBFAMILY 3 (G1).

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CC DR EMBL; AF059182; AAC1382.1; - .

DR HSSP; P10824; IBOF.

DR InterPro; IPR001019; Gprotein_alpha.

DR SMART; SM00275; G-alpha; 1.

DR PRINTS; PR00318; Gprotein_alpha.

DR PRODom; P000281; Gprotein_alpha.

DR SMART; SM00503; G-alpha; 1.

KW GTP-binding; transducer; Multigene family; ADP-ribosylation.

FT NP_BIND 200 204 GTP (BY SIMILARITY).

FT NP_BIND 269 272 GTP (BY SIMILARITY).

FT MOD_RES 178 178 ADP-RIBOSYL[1] (BY ACTION OF Cpx) (BY SIMILARITY).

FT SEQUENCE 354 AA; 41595 MW; C710502B037600E CRC64;

Query Match 82.6%; Score 15.37; DB 1; Length 354;
 Best Local Similarity 80.9%; Pred. No. 2. 5e-108; Mismatches 24; Indels 0; Gaps 0;

Matches 284; Conservative 43; Mismatches 24; Indels 0; Gaps 0;

Qy 9 CCLSEEEAKEARRINDELETERHYRDKDRARRELKLLLTGSGSKSFPIKOMRIIHGSYS 68

Db 4 CCLSAEEKKESQRISAEERQRLRDKDARRELKLLLTGSGSKSFPIKOMRIIHGSYS 63

Qy 129 VDAIKS1WNPQIQCYDRREYQLDSTSKYLNDLDRRAVPAYLPTQDYLVRVPTG 188

Db 124 VEAIKLWEDEGQECYDRREYQLDSTSKYLNDLDRRAVPAYLPTQDYLVRVPTG 183

Qy 189 IIEYPFDLQSVFMRMVQGQSERRKWICFENVTSMFLVSEYDQVLVSEEDNENRM 248

Db 184 IIEYPFDLLENIFRMDVGGQSERRKWICFENVTSMFLVSEYDQVLVSEEDNENRM 243

Qy 249 EESKAFLRTITYPWFQNSVILFLNKDLIEEKIMSHLYDYPEPDGPORDAQAREF 308

Db 244 EESKAFLRTITYPWFQNSVILFLNKDLIEEKIMSHLYDYPEPDGPORDAQAREF 303

RESULT 14

GB14_MOUSE STANDARD; PRT; 355 AA.

ID GB14_MOUSE

AC P30677;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Guanine nucleotide-binding protein, alpha-14 subunit.

GN GNA14 OR GNA14.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

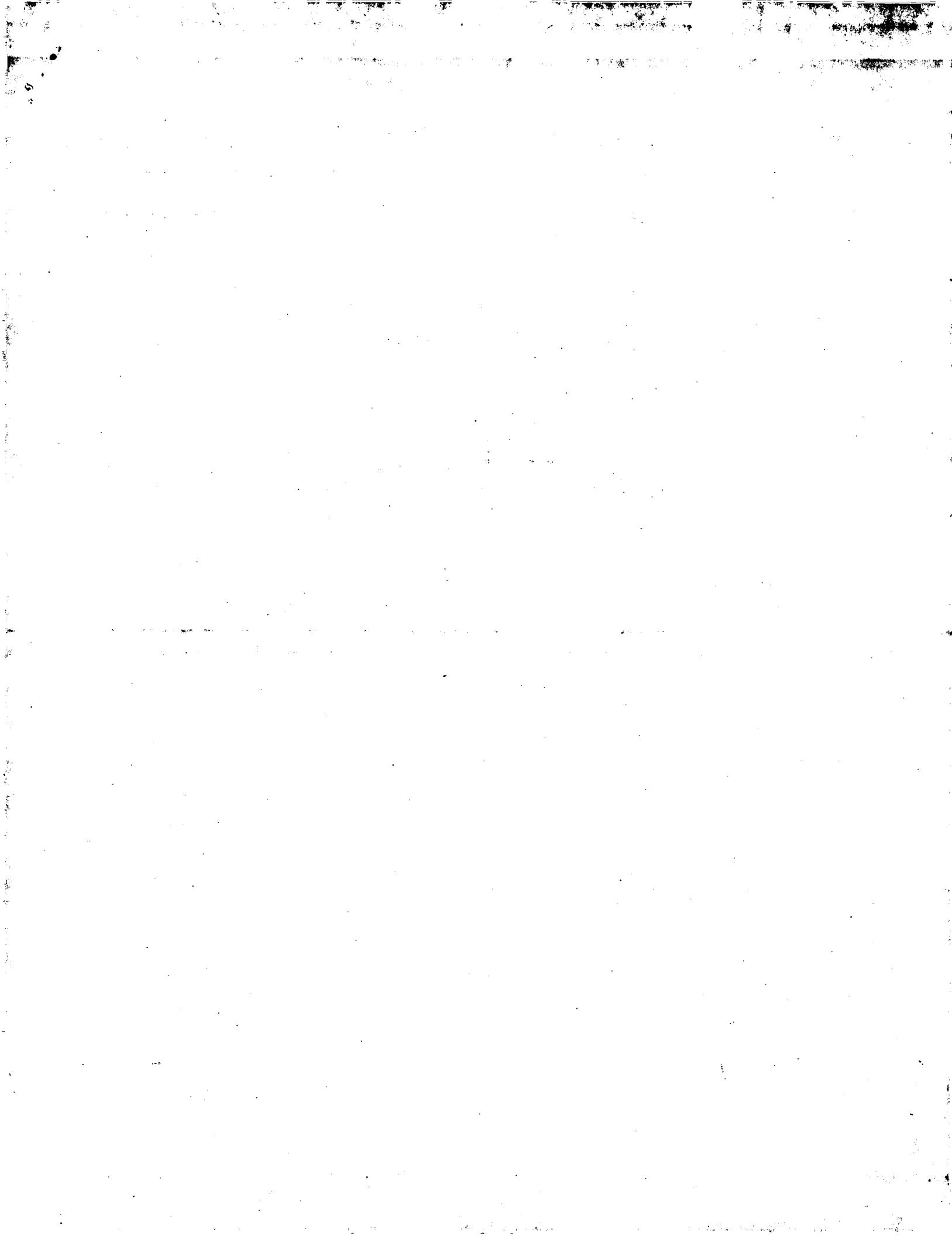
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

Db 121 QSVEALSLWADAGQECYQRREQLTOSAKYVDAVRIAEPYPLQDILURVRPT 180
Qy 187 TGIEYPFDLQSVIFRMVQGQRSERKWHCFCENVTSMFLVALSEYDQVLVESDEN 246
Db 181 TGIEYPFDLDSIFRMVQGQRSERKWHCFCENVTSMFLVALSEYDQVLVESDEN 240
Qy 247 RMEESKALFRPITYPWFQNSVILFLNKDLEEKIMSHLVDPFEDCPQDQAAR 306
Db 241 RMEESKALFRPITYPWFQNSVILFLNKDLEEKIMSHLVDPFEDGOKKDAQAR 300
Qy 307 EFLKMFVDINPDSKIKYSHFTCATDTENTRFVAAVKOTITLQNLKEYNLV 359
Db 301 EFLKMFVDINPDPDKITSHFTCATDTENTRFVAAVKOTITLQNLKEYNLV 353

Search completed: June 30, 2003, 16:16:29
Job time : 13 secs



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OM protein - protein search, using sw mode1

Run on: June 30, 2003, 16:12:56 ; Search time 80 Seconds
 (without alignments)
 924.636 Million cell updates/sec

Title: US-09-899-295-2

Perfect score: 1860

Sequence: 1 MTLESTMACCLSEEKAREARR..... VFAAVRKDTILQLNLKEYNLV 359

Scoring table: BLOSUM62

gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0.8
 Maximum Match 0.0%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_Plant:*

11: sp_rabbit:*

12: sp_rabbit:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriophage:*

17: SP_archeap:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1849	99.4	359	4 Q9BZB9
2	1656	89.6	359	11 Q91X95
3	1544	83.0	353	5 P91955
4	1532	82.4	353	5 Q9U473
5	1524	81.9	355	11 Q8T3X9
6	1513	81.3	355	5 Q17386
7	1504	80.9	353	5 Q9NL92
8	1498	80.5	353	5 Q8TP6P
9	1439	77.4	360	5 Q8WSUB
10	1430	76.9	353	5 Q9NFZ0
11	1291	69.4	303	5 Q8T3G5
12	1152.5	62.0	305	5 Q9Y207
13	1122.5	60.3	335	5 Q9XZV4
14	1112	59.5	279	5 Q91C78
15	1055	56.7	374	6 Q9TU29
16	902	48.5	353	3 Q8TGAA

RESULTS

1

RESULT 1

Q9BZB9

PRELIMINARY; PRT: 359 AA.

ID Q9BZB9; DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE G_alpha_q protein (Guanine nucleotide binding protein alpha q).

GN GNAQ.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88366708; PubMed=9700850;

RA Gabieta J., Dianasekaran N., Rao A.K.;

RT "G alpha q cDNA sequence from human platelets.";

RL Thromb. Res. 91:29-32(1998).

[2]

RP SEQUENCE FROM N.A.

RA Gabieta J., Dianasekaran N., Rao A.K.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

[3]

SEQUENCE FROM N.A.

RA Puri H.L., III, Ikeda S.R., Atonstam R.S.;

RT "Homo sapiens guanine nucleotide binding protein (G protein) alpha q (GNAQ)." Puri H.L., III, Ikeda S.R., Atonstam R.S.;

RT Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL: AF229284; AAG1117_1; -

EMBL: AF093896; AAM12610_1; -

DR HSSP: P10824; IBOF: Inter-Pro; IPR001019; Gprotein_alpha.

DR Pfam: PF00503; G-alpha; 1.

DR PRINTS: PRO0318; GPROTEINA.

DR Prodom: PRO00281; Gprotein_alpha; 1.

DR SMART: SM00275; G-alpha; 1.

SQ SEQUENCE 359 AA; 42142 MW; 6F69C4F617DF47C7 CRC64;

Query Match Best Local Similarity 99.4%; Score 1849; DB 4; Length 359;
Matches 357; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTLESIMACCLSEEKEARRINDELERHRDKRARRELKLILLGTGSGSKSF1K0MR 60
Db 61 IHGSGYSDBDKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 60
Qy 61 IHGSGYSDBDKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 60
Db 61 IHGSGYSDBDKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 60
Qy 121 VSAFNPYVDAIKSLWNPDGQIQCYDRREYQLSDTSTKYLNDLDRVADPAVPTQDVL 180
Db 121 VSAFNPYVDAIKSLWNPDGQIQCYDRREYQLSDTSTKYLNDLDRVADPAVPTQDVL 180
Qy 181 RVRYPTTGCIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 240
Db 181 RVRYPTTGCIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 240
Qy 241 ESDNENRMEESKALEFRTITYPWFQNSVYFLNKDLIEEKIMSHLYDYPEYDQOR 300
Db 241 ESDNENRMEESKALEFRTITYPWFQNSVYFLNKDLIEEKIMSHLYDYPEYDQOR 300
Qy 301 DAQAREFILKMFVLDNPDSK1IYSHFTCATDTENIRFVFAVKTDLQLNKEYLV 359
Db 301 DAQAREFILKMFVLDNPDSK1IYSHFTCATDTENIRFVFAVKTDLQLNKEYLV 359
RESULT 2
Q9IX95 PRELIMINARY; PRT; 359 AA.
ID Q9IX95 PRELIMINARY; PRT; 359 AA.
AC 09IX95: PRELIMINARY; PRT; 359 AA.
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to guanine nucleotide binding protein, alpha 11.
GN GNAII.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.
OX NCBI_TAXID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EML; BC01169; AAH1169.1; -
DR MGD; MGI:95766; GnaII.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha.
DR Prodrom; PDD00281; Gprotein_alpha; 1.
DR SMART; SM00725; G-alpha; 1.
SQ SEQUENCE 353 AA; 41497 MW; C1C57783B3D2D516 CRC64;

Query Match Best Local Similarity 83.0%; Score 144; DB 5; Length 353;
Matches 293; Conservative 28; Mismatches 32; Indels 0; Gaps 0;

Qy 7 MACCLSEEKEARRINDELERHRDKRARRELKLILLGTGSGSKSF1K0RIIHQG 66
Db 1 MACCLSEEKEQKRNQETEQRKDRARRELKLILLGTGSGSKSF1K0RIIHQG 66
Qy 67 YSDDEKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 126
Db 61 YSDDEKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 126
Qy 127 PYWDAIKSLWNPDGQIQCYDRREYQLSDTSTKYLNDLDRVADPAVPTQDVL 186
Db 121 PYWDAIKSLWNPDGQIQCYDRREYQLSDTSAKYLNDLDRVADPAVPTQDVL 180
Qy 187 TGIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 246
Db 181 TGIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 246
Qy 1 MTLESIMACCLSEEKEARRINDELERHRDKRARRELKLILLGTGSGSKSF1K0MR 60
Db 1 MTLESIMACCLSEEKEARRINDELERHRDKRARRELKLILLGTGSGSKSF1K0MR 60
Qy 61 IHGSGYSDBDKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 120
Db 61 IHGSGYSDBDKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 120
Qy 121 VSAFNPYVDAIKSLWNPDGQIQCYDRREYQLSDTKYLNDLDRVADPAVPTQDVL 180
Db 121 VSAFNPYVDAIKSLWNPDGQIQCYDRREYQLSDTKYLNDLDRVADPAVPTQDVL 180
Qy 181 RVRYPTTGCIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 240
Db 181 RVRYPTTGCIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 240
RESULT 3
P91955 PRELIMINARY; PRT; 353 AA.
ID P91955 PRELIMINARY; PRT; 353 AA.
AC P91955; PRELIMINARY; PRT; 353 AA.
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Gg protein alpha subunit.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicera; Merostomata; Xiphosura;
OC Limulida; Limulus.
OX NCBI_TAXID=6850;
RN [1]
RP SEQUENCE FROM N.A.
RC RA
DR PT
DR RT
DR RT
DR RL
DR Invert. Neurosci. 0:0(1997).
EMBL; U88586; AAB8510.1;
DR HSSP; P10824; IBOF;
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
DR PR00318; GPROTEINA.
DR PDD00281; Gprotein_alpha; 1.
DR SMART; SM00725; G-alpha; 1.
SQ SEQUENCE 353 AA; 41497 MW; C1C57783B3D2D516 CRC64;

Query Match Best Local Similarity 83.0%; Score 144; DB 5; Length 353;
Matches 293; Conservative 28; Mismatches 32; Indels 0; Gaps 0;

Qy 7 MACCLSEEKEARRINDELERHRDKRARRELKLILLGTGSGSKSF1K0RIIHQG 66
Db 1 MACCLSEEKEQKRNQETEQRKDRARRELKLILLGTGSGSKSF1K0RIIHQG 66
Qy 67 YSDDEKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 126
Db 61 YSDDEKRGFTKLVYQIFTAMQAMIRAMDTLKIPIKYBHNKAHQALREVDEK 126
Qy 127 PYWDAIKSLWNPDGQIQCYDRREYQLSDTSTKYLNDLDRVADPAVPTQDVL 186
Db 121 PYWDAIKSLWNPDGQIQCYDRREYQLSDTSAKYLNDLDRVADPAVPTQDVL 180
Qy 187 TGIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 246
Db 181 TGIEYPDQLQSVIFRMYDVGGRSERRKWICFENVISIMFLVALSEYDQVL 246
Qy 307 EFTLKMFDLNPDSK1IYSHFTCATDTENIRFVFAVKTDLQLNKEYLV 359
Db 301 EFTLKMFDLNPDSK1IYSHFTCATDTENIRFVFAVKTDLQLNKEYLV 359
RESULT 4
Q90473 PRELIMINARY; PRT; 353 AA.
ID Q90473 PRELIMINARY; PRT; 353 AA.
AC Q90473; PRELIMINARY; PRT; 353 AA.
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

QY 127 PYVDATKSLNDPGIQECYDRREYQVLSTKYYLNDLDRVADPAVLPTQDVLVRVPT 186
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 121 PYVEAKLWADAGIQECYDRREYQVLSTKYYLNDLDRVADPAVLPTQDVLVRVPT 180
 QY 187 TGILEYPFDIQLQSVIFRMVDVGQSERRKWICFENVTSMFLVALSEYDQVLVSDEN 246
 Db 181 TGILEYPFDIQLQSVIFRMVDVGQSERRKWICFENVTSMFLVALSEYDQVLVSDEN 240
 QY 247 RMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMYSHLVDFPEYDGPQAAR 306
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 241 RMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMYSHLVDFPEYDGPQAAR 300
 QY 307 EFLIKMFVLDNPDSKIKIYSHFTCATDTENIRFVAAVKTILQNLKEYNL 358
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 301 EFLIKMFVLDNPDSKIKIYSHFTCATDTENIRFVAAVKTILQNLKEYNL 352

RESULT 9

Q8WSUB PRELIMINARY; PRT; 360 AA.

ID Q8WSUB; PRELIMINARY; PRT; 360 AA.

DT 01-MAR-2002 (TREMBrel. 20, Created)

DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBrel. 21, Last annotation update)

DE G protein alpha subunit q class.

GN HRGQ.

OS Halocynthia roretzii (Sea squirt).

OC Eukaryota; Metazoa; Chordata; Urochordata; Asciidae; Stolidobranchia; Pyuridae; Halocynthia.

OC NCBI_TaxID=7729;

RN [1]

RP SEQUENCE FROM N.A.

RA Iwata T., Kandhara K., Watari A., Ohkuma M., Tsuda M.;
 "Cloning and expression patterns of G proteins in the larvae of
 Halocynthia roretzii"; Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB047034; BA079199; 1; -.

DR InterPro; IPR001019; Gprotein_alpha.

DR PRINTS; PR00318; GPROTEINA.

DR PRODOM; PD000281; Gprotein_alpha; 1.

DR SMART; SM00275; G_alpha; 1.

DR SEQUENCE 360 AA; 42571 MW; AACFB6AE3C56DC9 CRC64;

Query Match 76.1%; Score 1430; DB 5; Length 353; Matches 268; Conservative 39; Mismatches 45; Indels 0; Gaps 0;

QY 7 MACCSEEAKARRDEIEHRHRDKDRARRELKLLGIGECKSKTFIKOMRITHSG 66
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 61 YSDDDRGKGYIYLVFGQFIMANOSMKTAMDMLRISYGGARDHAELABLUMSIDYETVTSFED 120
 QY 127 PYVDATKSLNDPGIQECYDRREYQVLSDSTKYYLNDLDRVADPAVLPTQDVLVRVPT 186
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 121 PYLSAKTILWADTGQECYDRREYQVLSDTAKIYSLDLEIEQADYLPSQDILRARVPT 180
 QY 187 TGILEYPFDIQLQSVIFRMVDVGQSERRKWICFENVTSMFLVALSEYDQVLVSDEN 246
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 181 TGILEYPFDIQLQSVIFRMVDVGQSERRKWICFENVTSMFLVALSEYDQVLVSDEN 240
 QY 247 RMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMYSHLVDFPEYDGPQAAR 306
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 241 RMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMYSHLVDFPEYDGPQAAR 300
 QY 307 EFLIKMFVLDNPDSKIKIYSHFTCATDTENIRFVAAVKTILQNLKEYNL 358
 |||:|||:|||:|||:|||:|||:|||:|||:
 Db 301 QFVLUKYLAANPDRQCYSHFTCATDTENIRFVAAVKTILQNLKEYNL 352

RESULT 11

Q8T355 PRELIMINARY; PRT; 303 AA.

ID Q8T355; PRELIMINARY; PRT; 303 AA.

AC Q9N7Z0; PRELIMINARY; PRT; 353 AA.

DT 01-NOT-2000 (TREMBrel. 15, Created)

DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

DE Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).

OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).

OC Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Calliphora.

OC NCBI_TaxID=7373;

RN [1]

RP SEQUENCE FROM N.A.

RA Schullz S., Huber A., Schwab K., Paulsen R.;
 "A novel Ggamma isolated from Drosophila constitutes a visual G protein gamma subunit of the fly compound eye.";
 Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ750443; CAB76453; 1; -.

DR HSSP; P10824; IBOF.

DR Inta-Pro; IPR001019; Gprotein_alpha.

DR Pfam; PF00503; G-alpha; 1.

DR PRINTS; PR00318; GPROTEINA.

DR PRODOM; PD000281; Gprotein_alpha; 1.

DR SMART; SM00275; G-alpha; 1.

DR SEQUENCE 353 AA; 41235 MW; FFF7799774C02072E CRC64;

Query Match 76.1%; Score 1430; DB 5; Length 353; Matches 268; Conservative 39; Mismatches 45; Indels 0; Gaps 0;

QY 7 MACCSEEAKARRDEIEHRHRDKDRARRELKLLGIGECKSKTFIKOMRITHSG 66
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 61 YSDDDRGKGYIYLVFGQFIMANOSMKTAMDMLRISYGGARDHAELABLUMSIDYETVTSFED 120
 QY 127 PYVDATKSLNDPGIQECYDRREYQVLSDSTKYYLNDLDRVADPAVLPTQDVLVRVPT 186
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 121 PYLSAKTILWADTGQECYDRREYQVLSDTAKIYSLDLEIEQADYLPSQDILRARVPT 180
 QY 187 TGILEYPFDIQLQSVIFRMVDVGQSERRKWICFENVTSMFLVALSEYDQVLVSDEN 246
 |||:|||:|||:|||:|||:|||:|||:|||:
 Db 181 TGILEYPFDIQLQSVIFRMVDVGQSERRKWICFENVTSMFLVALSEYDQVLVSDEN 240
 QY 247 RMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMYSHLVDFPEYDGPQAAR 306
 |||:|||:|||:|||:|||:|||:|||:|||:
 Db 241 RMEESKALFRITITYPWFOQNSVILFLNKDLLEEKIMYSHLVDFPEYDGPQAAR 300
 QY 307 EFLIKMFVLDNPDSKIKIYSHFTCATDTENIRFVAAVKTILQNLKEYNL 358
 |||:|||:|||:|||:|||:|||:
 Db 301 QFVLUKYLAANPDRQCYSHFTCATDTENIRFVAAVKTILQNLKEYNL 352

RESULT 11

Q8T355 PRELIMINARY; PRT; 303 AA.

ID Q8T355; PRELIMINARY; PRT; 303 AA.

AC Q9N7Z0; PRELIMINARY; PRT; 353 AA.

DT 01-JUN-2002 (TREMBrel. 21, Created)

DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE C. elegans EGL-30 protein (corresponding sequence M01D7.7b).

GN EGL-30.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae; Peledorinae; Caenorhabditis.

OC NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC	STRAIN=BRISTOL N2;	DR	Pfam:PF00503; G-alpha; 1.
RX	MEDLINE:9906613; PubMed=9851916;	RP	PRINTS; PRO018; GPROTEINA.
RA	Waterson R.;	DR	PRODOM; PD000281; Gprotein_alpha; 1.
RT	"Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium. ";	DR	SMART; SW00275; G-alpha; 1.
RL	Science 282:2012-2018(1998).	FT	NON_TER 1
[2]		FT	NON_TER 1
RN	SEQUENCE FROM N.A.	FT	NON_TER 1
RP	STRAIN=BRISTOL N2;	FT	NON_TER 1
RC	Gattung S., Goela D.;	FT	NON_TER 1
RA	"The sequence of <i>C. elegans</i> cosmids M01D7. ";	FT	NON_TER 1
RL	Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.	FT	NON_TER 1
RN	[13]	FT	NON_TER 1
RP	SEQUENCE FROM N.A.	FT	NON_TER 1
RC	STRAIN=BRISTOL N2;	FT	NON_TER 1
RA	Waterson R.;	FT	NON_TER 1
RL	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.	FT	NON_TER 1
DR	EMBL; AR003739; AAM15531; -.	FT	NON_TER 1
SQ	SEQUENCE 303 AA; 35807 MW; 12B5A76956116D28 CRC64;	FT	NON_TER 1
Query	Match 69.4%; Score 1291; DB 5; Length 303;	DR	PF00503; G-alpha; 1.
Best Local Similarity 81.8%; Pred. No. 8e-93; Matches 248; Conservative 20; Mismatches 31; Indels 2; Gaps 1;	RP	PRINTS; PRO018; GPROTEINA.	
QY	59 MRLHSGSISDEDRGFTKLWQNIIFTAMQAMRAMDTLKIPIY-KYENKAHQLVQE 116	DR	PRODOM; PD000281; Gprotein_alpha; 1.
Db	1 MRLHSGSISDEDRGFTKLWQNIIFTAMQAMRAMDTLKIPIY-KYENKAHQLVQE 116	DR	SMART; SW00275; G-alpha; 1.
QY	117 DVEKVSAPENPVYDAIKSLWNPQTCYCDRREYOLSDSTKYLNDLDRDPAVLPTQ 176	DR	NON_TER 1
Db	61 DFEVSITSEDPVWYIKEWEDSICQECYRRLQYLDKSYLSDSAKYLSDLRKICAPNVP 120	DR	NON_TER 1
QY	177 QDILRVRYPTGIEYPFDLQFIRMVQDVGGRSERRKWHCPENVISIMLVALSEVD 236	DR	NON_TER 1
Db	121 QDILRVRYPTGIEYPFDLQFIRMVQDVGGRSERRKWHCPENVISIMLVALSEVD 180	DR	NON_TER 1
QY	237 QLVESDNRMERMEKSKALFRITYPWCONSSVILFLNKDLFEKTMYSHVYDPEVD 296	DR	NON_TER 1
Db	181 QVLVCDNERNMEEKSALKFRITYPWCONSSVILFLNKDLFEKTMYSHVYDPEVD 240	DR	NON_TER 1
QY	297 GPRQDAQARREFILKMFVLNPDSDKIYSHFTCATDENTRFAAVKDTIQLNKEY 356	DR	NON_TER 1
Db	241 GPRDPIAAREFLKMFVLNPDSDKIYSHFTCATDENTRFAAVKDTIQLNKEY 300	DR	NON_TER 1
QY	357 NLV 359	DR	NON_TER 1
Db	301 NLV 303	DR	NON_TER 1
RESULT 12		DR	NON_TER 1
Q9Y207	PRELIMINARY; PRT; 305 AA.	DR	NON_TER 1
ID	Q9Y207	DR	NON_TER 1
AC	Q9Y207;	DR	NON_TER 1
DT	01-NOV-1999 (TREMBLrel. 12, Created)	DR	NON_TER 1
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	DR	NON_TER 1
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	DR	NON_TER 1
DE	G protein a subunit 3 (Fragment).	DR	NON_TER 1
OS	Hydra magnipapillata (Hydra).	DR	NON_TER 1
OC	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoida; Anthomedusae;	DR	NON_TER 1
OC	Hydridae; Hydra.	DR	NON_TER 1
OX	NCBI_TaxID=6047;	DR	NON_TER 1
RN		DR	NON_TER 1
RP	SEQUENCE FROM N.A.	DR	NON_TER 1
RX	MEDLINE:9811957; PubMed=9459489;	DR	NON_TER 1
RA	Seack J., Kruse M., Mueller W.E.G.;	DR	NON_TER 1
RT	"Evolutionary analysis of G-protein in early metazoans: Cloning of alpha- and beta-subunits from the sponge <i>Geodia cydonium</i> .";	DR	NON_TER 1
RL	Biochim. Biophys. Acta 1401:93-103(1998).	DR	NON_TER 1
DR	EMBL; Y14248; CAB3527.1; -.	DR	NON_TER 1
DR	P04896; 1AZT	DR	NON_TER 1
DR	InterPro; IPR001019; Gprotein_alpha.	DR	NON_TER 1
DR	PF00503; G-alpha; 1.	DR	NON_TER 1
DR	PRINTS; PR00318; GPROTEINA.	DR	NON_TER 1
DR	PRODOM; PD000281; Gprotein_alpha; 1.	DR	NON_TER 1
DR	SMART; SW00275; G-alpha; 1.	DR	NON_TER 1
SQ	SEQUENCE 355 AA; 41363 MW; 6828029643F2CE91 CRC64;	DR	NON_TER 1
Query	Match 60.3%; Score 1122.5; DB 5; Length 355;	DR	NON_TER 1
Best Local Similarity 61.4%; Pred. No. 1.4e-79; Matches 215; Conservative 51; Mismatches 83; Indels 1; Gaps 1;	DR	NON_TER 1	
QY	7 MACCLSEGAKEATRINDETERHYRDRDARBLKLILLGEGSKSTFIKOMRIHGG 66	DR	NON_TER 1
Db	1 MSCLLSEEBERLQRINTRINRELQDHDAKKEIKLILLGEGSKSTFIKOMRIHGG 60	DR	NON_TER 1

13 CLESEDEKAARVQDIEIRLLEHRRQVRGEKLKLIGTGESEKSTFIKOMRIHAGYSE 72
 QY EDKRGFTKLYQNTETAMOMIRAMDTLKPKYKHNKAQOLYREVDYEVKSAFENPV 129
 Db EDRKDFRPLFONITFLSVQKIEAMDRQPSRSESKHLASLYMSQDPYKVNTFETRA 132
 QY DAIKSLWNDEGIQECYDRREYQLSDSTKYLNDLDRVADPAULPTQDQVLVRVRYPTGI 189
 130 LAVOSILWRDAGVRACYERRREFHILDSAVVYLSHLERIAEGYVPTAODVLRSRMPPTGI 192
 Db 133
 QY IYEPDLQSVIFRMWDVGGORSERRKWIHOFENVNISMEFVALSBYDQWLVESONENRME 249
 190 NEYCFSVQKINLRIVDGGOKSERKKWICHEFDYALIFASLSPEYDQCLEENQENRQ 252
 Db 193
 QY ESKALFRITITYPNFONSSYTLFLNKDKLEEKIMYSHUDYFPEYDGQDQAARETI 309
 250 253 ESLAIFGTYALPWRATSTYLFLNKTDIEKDVKPHTIATYFFGFRGPPDPPEAKRTI 312
 Db 310 LKMFVDL----NPD-----DKIYSHFTCATTENIRFVFAVKDITLQLNLIKEYN 357
 QY 131 LELYTRVYAGAAGPDGDKGPRSRRLFSHYTCAOTNIRKVKDVRSVLRVLDIN 372
 Db 313
 QY 358 LV 359
 Db 373 LL 374

Search completed: June 30, 2003, 16:17:58
 Job time : 83 secs